GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 2, 2001, 23:29:13 ; Search time 1817.54 Seconds
(without alignments)
4212.372 Million cell updates/sec

Title: US-09-380-276A-7
Perfect score: 1496
Sequence: 1 gggaacgtagaactctccaa.....aaaaaaaaaaaaaaaaaaaa 1496

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1118133 seqs, 2558875100 residues

Total number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba1:*
2: gb_ba2:*
3: gb_om:*
4: gb_ov:*
5: gb_ph:*
6: gb_pl1:*
7: gb_pl2:*
8: gb_pr1:*
9: gb_pr2:*
10: gb_pr3:*
11: gb_ro:*
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13: gb_un:*
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80: gb_vi2:*
81: gb_pat1:*
82: gb_pat2:*
83: em_htg0:*
84: gb_htg24:*
85: gb_pr8:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1421.4	95.0	1489	34	AF167555	AF167555 Homo sapi
	2	1359.2	90.9	1364	8	AB040434	AB040434 Homo sapi
	3	744.2	49.7	3964	11	AB040432	AB040432 Mus muscu
	4	741	49.5	1678	11	AF167552	AF167552 Mus muscu
	5	692.6	46.3	1075	11	AF173166	AF173166 Mus muscu
	6	586.6	39.2	143608	73	AL161422	AL161422 Homo sapi
	7	586.6	39.2	178256	72	AL139080	AL139080 Homo sapi
	8	460.8	30.8	744	11	AB040433	AB040433 Mus muscu
	9	460.8	30.8	886	11	AF167553	AF167553 Mus muscu
	10	326.6	21.8	591	11	AF167554	AF167554 Mus muscu
c	11	73	4.9	188351	73	AL353136	AL353136 Homo sapi
c	12	73	4.9	205736	63	AC023560	AC023560 Homo sapi
	13	65.4	4.4	205736	63	AC023560	AC023560 Homo sapi
	14	64	4.3	3618	11	RNU67080	U67080 Rattus norv
c	15	63.8	4.3	6105	12	ASPDXA3H	X85119 Artificial
c	16	63.8	4.3	6113	12	ASPDXA3C	X85118 Artificial
c	17	60.2	4.0	178273	54	AC005308	AC005308 Plasmodiu
c	18	59.6	4.0	202872	58	AC016160	AC016160 Homo sapi
	19	59.2	4.0	13007	31	BMU07224	U07224 Brugia mala
	20	59	3.9	163443	54	AC006280	AC006280 Plasmodiu
c	21	59	3.9	196149	54	AC004709	AC004709 Plasmodiu

c	22	58.6	3.9	318221	84	PFMAL13P3	AL049184 Plasmodiu
	23	58.2	3.9	899	31	AF273837	AF273837 Caenorhab
	24	57.2	3.8	2260	10	AF116602	AF116602 Homo sapi
c	25	56.6	3.8	180144	63	AC023429	AC023429 Homo sapi
	26	56.2	3.8	1678	53	HSHIRIP4	Y13350 Homo sapien
	27	56	3.7	1775	6	AB029462	AB029462 Salix gil
	28	56	3.7	2390	10	AF090900	AF090900 Homo sapi
	29	56	3.7	4435	4	XLMILZ	Z97214 Xenopus lae
c	30	56	3.7	205429	54	AC005506	AC005506 Plasmodiu
	31	55.6	3.7	1081	4	OLA250403	AJ250403 Oryzias l
	32	55.6	3.7	2207	34	AK027166	AK027166 Homo sapi
	33	55.4	3.7	447	34	AK026855	AK026855 Homo sapi
	34	55.2	3.7	1261	7	AF243180	AF243180 Lycopersi
c	35	55	3.7	2982	32	DDISGSPA	M33862 Dictyosteli
	36	54.8	3.7	470	31	AF177908	AF177908 Hydra vul
	37	54.8	3.7	1582	81	A77033	A77033 Sequence 10
	38	54.8	3.7	1582	81	A77035	A77035 Sequence 12
	39	54.6	3.6	1596	32	LTACT1596	X96512 L.terrestri
c	40	54.6	3.6	153166	67	AC048357	AC048357 Homo sapi
	41	54.6	3.6	321003	84	PFMAL4P3	AL035476 Plasmodiu
	42	54.4	3.6	1068	77	CNS01E0R	AL139948 Anopheles
c	43	54.4	3.6	3138	81	A21625	A21625 expression
	44	54.4	3.6	3720	11	AF160502	AF160502 Mus muscu
	45	54.4	3.6	4615	32	DDIMANA	M82822 Dictyosteli

ALIGNMENTS

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RESULT   1
AF167555
LOCUS       AF167555     1489 bp    mRNA            PRI       25-MAY-2000
DEFINITION  Homo sapiens TAJ-alpha mRNA, complete cds.
ACCESSION   AF167555
VERSION     AF167555.1  GI:8071643
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1489)
  AUTHORS   Eby,M.T., Jasmin,A., Kumar,A., Sharma,K. and Chaudhary,P.M.
  TITLE     TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
            Activates the c-Jun N-terminal Kinase Pathway and Mediates
            Caspase-independent Cell Death
  JOURNAL   J. Biol. Chem. 275 (20), 15336-15342 (2000)
   PUBMED   10809768
REFERENCE   2  (bases 1 to 1489)
  AUTHORS   Chaudhary,P.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-JUL-1999) Internal Medicine, UT Southwestern Medical
            Center, 5323 Harry Hines Blvd., Dallas, TX 75235-8593, USA
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
     CDS             65. .1336
                     /codon_start=1
                     /product="TAJ-alpha"
                     /protein_id="AAF71828.1"
                     /db_xref="GI:8071644"
                     /translation="MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSG
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                     KANCSATSDAICGDCLPGFYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIAS
                     TASSPRDTALAAVICSALATVLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNETEL
                     SCFDRPQLHEYAHRACCQCRRDSVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAAS
                     LQARNAGPAGEMVPTFFGSLTQSICGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDI
                     HSLNPELESSTSLDSNSSQDLVGGAVPVQSHSENFTAATDLSRYNNTLVESASTQDAL
                     TMRSQLDQESGAVIHPATQTSLQVRQRLGSL"
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ORIGIN
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  Best Local Similarity  98.8%;  Pred. No. 4.1e-287;
  Matches 1443;  Conservative    0;  Mismatches   16;  Indels    2;  Gaps    1;

Qy       7 gtagaactctccaacaataaatacatttgataagaaagatggctttaaaagtgctactag 66
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      27 GAAGAACTCTCCAACAATAAATACATTTGATAAGAAAGATGGCTTTAAAAGTGCTACTAG 86

Qy      67 aacaagagaaaacgtttttcactcttttagtattactaggctatttgtcatgtaaagtga 126
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Db      87 AACAAGAGAAAACGTTTTTCACTCTTTTAGTATTACTAGGCTATTTGTCATGTAAAGTGA 146

Qy     127 cttgtgaaacaggagactgtagacagcaagaattcagggatcggtctggaaactgtgttc 186
           |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     147 CTTGTGAATCAGGAGACTGTAGACAGCAAGAATTCAGGGATCGGTCTGGAAACTGTGTTC 206

Qy     187 cctgcaaccagtgtgggccaggcatggagttgtctaaggaatgtggcttcggctatgggg 246
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Db     207 CCTGCAACCAGTGTGGGCCAGGCATGGAGTTGTCTAAGGAATGTGGCTTCGGCTATGGGG 266

Qy     247 aggatgcacagtgtgtgacgtgccggctgcacaggttcaaggaggactggggcttccaga 306
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db     267 AGGATGCACAGTGTGTGGCGTGCCGGCTGCACAGGTTCAAGGAGGACTGGGGCTTCCAGA 326

Qy     307 aatgcaagccctgtctggactgcgcagtggtgaaccgctttcagaaggcaaattgttcag 366
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Db     327 AATGCAAGCCCTGTCTGGACTGCGCAGTGGTGAACCGCTTTCAGAAGGCAAATTGTTCAG 386

Qy     367 ccaccagtgatgccatctgcggggactgcttgccaggattttataggaagacgaaacttg 426
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Qy     427 tcggctttcaagacatggagtgtgtgccttgtggagaccctcctcctccttacgaaccgc 486
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Qy     487 actgtgccagcaaggtcaacctcgtgaagatcgcgtccacggcctccagcccacgggaca 546
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Db     507 ACTGTGCCAGCAAGGTCAACCTCGTGAAGATCGCGTCCACGGCCTCCAGCCCACGGGACA 566

Qy     547 cggcgctggctgccgttatctgcagcgctctggccaccgtcctgctggccctgctcatcc 606
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Db     567 CGGCGCTGGCTGCCGTTATCTGCAGCGCTCTGGCCACCGTCCTGCTGGCCCTGCTCATCC 626

Qy     607 tctgtgtcatctattgtaagagacagtttatggagaagaaacccagctggtctctgcggt 666
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Db     627 TCTGTGTCATCTATTGTAAGAGACAGTTTATGGAAAAGAAACCCAGCTGGTCTCTGCGGT 686

Qy     667 cacaggacattcagtacaacggctctgagctgtcgtgtcttgacagacctcagctccacg 726
           ||||||||||||||||||   |||||||||||| ||||||||||||||||||||||||||
Db     687 CACAGGACATTCAGTACAACGAGACTGAGCTGTCGTGTTTTGACAGACCTCAGCTCCACG 746

Qy     727 aatatgcccacagagcctgctgccagtgccgccgtgactcagtgcagacctgcgggccgg 786
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Db     747 AATATGCCCACAGAGCCTGCTGCCAGTGCCGCCGTGACTCAGTGCAGACCTGCGGGCCGG 806

Qy     787 tgcgcttgctcccatccatgtgctgtgaggaggcctgcagccccaacccggcgactcttg 846
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Qy     847 gttgtggggtgcattctgcagccagtcttcaggcaagaaacgcaggcccagccggggaga 906
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Qy     907 tggtgccgactttcttcggatccctcacgcagtccatctgtggcgagttttcagatgcct 966
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Db     927 TGGTGCCGACTTTCTTCGGATCCCTCACGCAGTCCATCTGTGGCGAGTTTTCAGATGCCT 986

Qy     967 ggcctctgatgcagaatcccatgggtggtgacaacatctctttttgtgactcttatcctg 1026
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Db     987 GGCCTCTGATGCAGAATCCCATGGGTGGTGACAACATCTCTTTTTGTGACTCTTATCCTG 1046

Qy    1027 aactcactggagaagacattcattctctcaatccagaacttgaaagctcaacgtctttgg 1086
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Qy    1087 attcaaatagcagtcaagatttggttggtggggctgttccagtccagtctcattctgaaa 1146
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Qy    1147 actttacagcagctactgatttatctagatataacaacacactggtagaatcagcatcaa 1206
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Qy    1267 cagccactcagacgtccctccaggtaaggcagcgactgggttccctgtgaacacagcact 1326
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Qy    1385 ttttttttgcatctttaataatttcttgtatgttgtagagtatgttttaaaataaattt 1444
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Db    1407 TTTTTTTTTGCATCTTTAATAATTTCTTATATGTTGTAGAGTATGTTTTAAAATAAATTT 1466

Qy    1445 caagtatttttttaaaaact 1465
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RESULT   2
AB040434
LOCUS       AB040434     1364 bp    mRNA            PRI       22-JUL-2000
DEFINITION  Homo sapiens mRNA for hTROY, complete cds.
ACCESSION   AB040434
VERSION     AB040434.1  GI:9392329
KEYWORDS    hTROY.
SOURCE      Homo sapiens cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Kojima,T., Morikawa,Y., Copeland,N.G., Gilbert,D.J., Jenkins,N.A.,
            Senba,E. and Kitamura,T.
  TITLE     TROY, a newly identified member of the tumor necrosis factor
            receptor superfamily, exhibits a homology with Edar and is
            expressed in embryonic skin and hair follicles
  JOURNAL   J. Biol. Chem. 275 (27), 20742-20747 (2000)
  MEDLINE   20347167
REFERENCE   2  (bases 1 to 1364)
  AUTHORS   Kojima,T. and Kitamura,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-MAR-2000) to the DDBJ/EMBL/GenBank databases. Tetsuo
            Kojima, Chugai Research Institute for Molecular Medicine, Inc.,
            Cytokine Research Program; 153-2 Nagai, Niihari, Ibaraki 300-4101,
            Japan (E-mail:kojimat@cimmed.com, Tel:81-298-306211,
            Fax:81-298-306270)
COMMENT     Sequence updated (06-Apr-2000).
FEATURES             Location/Qualifiers
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                     SCFDRPQLHEYAHRACCQCRRDSVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAAS
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ORIGIN


  Query Match             90.9%;  Score 1359.2;  DB 8;  Length 1364;
  Best Local Similarity   99.8%;  Pred. No. 4.1e-274;
  Matches 1361;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      9 agaactctccaacaataaatacatttgataagaaagatggctttaaaagtgctactagaa 68
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 AGAACTCTCCAACAATAAATACATTTGATAAGAAAGATGGCTTTAAAAGTGCTACTAGAA 60

Qy     69 caagagaaaacgtttttcactcttttagtattactaggctatttgtcatgtaaagtgact 128
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Qy    129 tgtgaaacaggagactgtagacagcaagaattcagggatcggtctggaaactgtgttccc 188
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Qy    189 tgcaaccagtgtgggccaggcatggagttgtctaaggaatgtggcttcggctatggggag 248
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Qy    249 gatgcacagtgtgtgacgtgccggctgcacaggttcaaggaggactggggcttccagaaa 308
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Qy    309 tgcaagccctgtctggactgcgcagtggtgaaccgctttcagaaggcaaattgttcagcc 368
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Qy    369 accagtgatgccatctgcggggactgcttgccaggattttataggaagacgaaacttgtc 428
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Db    361 ACCAGTGATGCCATCTGCGGGGACTGCTTGCCAGGATTTTATAGGAAGACGAAACTTGTC 420

Qy    429 ggctttcaagacatggagtgtgtgccttgtggagaccctcctcctcctcttacgaaccgcac 488
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Db    421 GGCTTTCAAGACATGGAGTGTGTGCCTTGTGGAGACCCTCCTCCTCCTTACGAACCGCAC 480

Qy    489 tgtgccagcaaggtcaacctcgtgaagatcgcgtccacggcctccagcccacgggacacg 548
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Qy    549 gcgctggctgccgttatctgcagcgctctggccaccgtcctgctggccctgctcatcctc 608
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GCGCTGGCTGCCGTTATCTGCAGCGCTCTGGCCACCGTCCTGCTGGCCCTGCTCATCCTC 600

Qy    609 tgtgtcatctattgtaagagacagtttatggagaagaaacccagctggtctctgcggtca 668
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Db    601 TGTGTCATCTATTGTAAGAGACAGTTTATGGAGAAGAAACCCAGCTGGTCTCTGCGGTCA 660

Qy    669 caggacattcagtacaacggctctgagctgtcgtgtcttgacagacctcagctccacgaa 728
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Db    661 CAGGACATTCAGTACAACGGCTCTGAGCTGTCGTGTTTTGACAGACCTCAGCTCCACGAA 720

Qy    729 tatgcccacagagcctgctgccagtgccgccgtgactcagtgcagacctgcgggccggtg 788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 TATGCCCACAGAGCCTGCTGCCAGTGCCGCCGTGACTCAGTGCAGACCTGCGGGCCGGTG 780

Qy    789 cgcttgctcccatccatgtgctgtgaggaggcctgcagccccaacccggcgactcttggt 848
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CGCTTGCTCCCATCCATGTGCTGTGAGGAGGCCTGCAGCCCCAACCCGGCGACTCTTGGT 840

Qy    849 tgtggggtgcattctgcagccagtcttcaggcaagaaacgcaggcccagccggggagatg 908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    841 TGTGGGGTGCATTCTGCAGCCAGTCTTCAGGCAAGAAACGCAGGCCCAGCCGGGGAGATG 900

Qy    909 gtgccgacttttcttcggatccctcacgcagtccatctgtggcgagttttcagatgcctgg 968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GTGCCGACTTTCTTCGGATCCCTCACGCAGTCCATCTGTGGCGAGTTTTCAGATGCCTGG 960

Qy    969 cctctgatgcagaatcccatgggtggtgacaacatctctttttgtgactcttatcctgaa 1028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CCTCTGATGCAGAATCCCATGGGTGGTGACAACATCTCTTTTTGTGACTCTTATCCTGAA 1020

Qy   1029 ctcactggagaagacattcattctctcaatccagaacttgaaagctcaacgtctttggat 1088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CTCACTGGAGAAGACATTCATTCTCTCAATCCAGAACTTGAAAGCTCAACGTCTTTGGAT 1080

Qy   1089 tcaaatagcagtcaagatttggttggtggggctgttccagtccagtctcattctgaaaac 1148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TCAAATAGCAGTCAAGATTTGGTTGGTGGGGCTGTTCCAGTCCAGTCTCATTCTGAAAAC 1140

Qy   1149 tttacagcagctactgatttatctagatataacaacacactggtagaatcagcatcaact 1208
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Db   1141 TTTACAGCAGCTACTGATTTATCTAGATATAACAACACACTGGTAGAATCAGCATCAACT 1200

Qy   1209 caggatgcactaactatgagaagccagctagatcaggagagtggcgctatcatccaccca 1268
          ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   1201 CAGGATGCACTAACTATGAGAAGCCAGCTAGATCAGGAGAGTGGCGCTGTCATCCACCCA 1260

Qy   1269 gccactcagacgtccctccaggtaaggcagcgactgggttccctgtgaacacagcactga 1328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GCCACTCAGACGTCCCTCCAGGTAAGGCAGCGACTGGGTTCCCTGTGAACACAGCACTGA 1320

Qy   1329 cttacagtagatcagaactctgttcccagcataagatttggggg 1372
          |||||||||||||||||||||||||||||||||||||||||||
Db   1321 CTTACAGTAGATCAGAACTCTGTTCCCAGCATAAGATTTGGGGG 1364
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RESULT   3
AB040432
LOCUS       AB040432     3964 bp    mRNA            ROD       22-JUL-2000
DEFINITION  Mus musculus mRNA for TROY, complete cds.
ACCESSION   AB040432
VERSION     AB040432.1  GI:9392325
KEYWORDS    TROY.
SOURCE      Mus musculus cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (sites)
  AUTHORS   Kojima,T., Morikawa,Y., Copeland,N.G., Gilbert,D.J., Jenkins,N.A.,
            Senba,E. and Kitamura,T.
  TITLE     TROY, a newly identified member of the tumor necrosis factor
            receptor superfamily, exhibits a homology with Edar and is
            expressed in embryonic skin and hair follicles
  JOURNAL   J. Biol. Chem. 275 (27), 20742-20747 (2000)
  MEDLINE   20347167
REFERENCE   2  (bases 1 to 3964)
  AUTHORS   Kojima,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-MAR-2000) to the DDBJ/EMBL/GenBank databases. Tetsuo
            Kojima, Chugai Research Institute for Molecular Medicine, Inc.,
            Cytokine Research Program; 153-2 Nagai, Niihari, Ibaraki 300-4101,
            Japan (E-mail:kojimat@cimmed.com, Tel:81-298-306211,
            Fax:81-298-306270)
FEATURES             Location/Qualifiers
     source          1. .3964
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                     /gene="Troy"
     CDS             127. .1377
                     /gene="Troy"
                     /note="a member of TNFR superfamily exhibits a homology
                     with Edar"
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                     /product="TROY"
                     /protein_id="BAB03267.1"
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                     RANCSHTSDAVCGDCLPGFYRKTKLVGFQDMECVPCGDPPPPYEPHCTSKVNLVKISS
                     TVSSPRDTALAAVICSALATVLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSEL
                     SCFDQPRLRHCAHRACCQYHRDSAPMYGPVHLIPSLCCEEARSSARAVLGCGLRSPTT
                     LQERNPASVGDTMPAFFGSVSRSICAEFSDAWPLMQNPLGGDSSLCDSYPELTGEDTN
                     SLNPENESAASLDSSGGQDLAGTAALESSGNVSESTDSPRHGDTGTVWEQTLAQDAQR
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BASE COUNT      984 a    958 c    980 g   1041 t      1 others
ORIGIN
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  Query Match           49.7%;  Score 744.2;  DB 11;  Length 3964;
  Best Local Similarity  74.7%;  Pred. No. 1.6e-145;
  Matches  948;  Conservative    0;  Mismatches  318;  Indels    3;  Gaps    1;

Qy     22 aataaatacatttgataagaaagatggctttaaaagtgctactagaacaagagaaaacgt 81
          |||||| || |||| | |||   |||||  | || || ||||    |||   ||    |
Db    104 AATAAACACGTTTGGTGAGAGCCATGGCACTCAAGGTCCTACCTCTACACAGGACGGTGC 163

Qy     82 ttttcactcttttagtattactaggctatttgtcatgtaaagtgacttgtgaaacaggag 141
          | ||| ||    |  | || ||| | |  || ||||||||||||| ||| ||||| ||||
Db    164 TCTTCGCTGCCATTCTCTTCCTACTCCACCTGGCATGTAAAGTGAGTTGCGAAACCGGAG 223

Qy    142 actgtagacagcaagaattcagggatcggtctggaaactgtgttccctgcaaccagtgtg 201
          | || || ||||| ||||||| ||||| |||||||||||||| | |||||| ||||| |
Db    224 ATTGCAGGCAGCAGGAATTCAAGGATCGATCTGGAAACTGTGTCCTCTGCAAACAGTGCG 283

Qy    202 ggccaggcatggagttgtctaaggaatgtggcttcggctatggggaggatgcacagtgtg 261
          | || |||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    284 GACCTGGCATGGAGTTGTCCAAGGAATGTGGCTTCGGCTATGGGGAGGATGCACAGTGTG 343

Qy    262 tgacgtgccggctgcacaggttcaaggaggactggggcttccagaaatgcaagccctgtc 321
          || | ||| ||| |||| |||||||||| |||||||| |||||||| || ||||| |||
Db    344 TGCCCTGCAGGCCGCACCGGTTCAAGGAAGACTGGGGTTTCCAGAAGTGTAAGCCATGTG 403

Qy    322 tggactgcgcagtggtgaaccgctttcagaaggcaaattgttcagccaccagtgatgcca 381
          ||||||  ||  |||||||||||||||||| ||| || || ||| ||||||||||||
Db    404 CGGACTGTGCGCTGGTGAACCGCTTTCAGAGGGCCAACTGCTCACACACCAGTGATGCTG 463

Qy    382 tctgcggggactgcttgccaggattttataggaagacgaaacttgtcggctttcaagaca 441
          |||||||||||||| ||||||||||||  ||||||| ||||| || || ||||||||||
Db    464 TCTGCGGGGACTGCCTGCCAGGATTTTACCGGAAGACCAAACTGGTTGGTTTTCAAGACA 523

Qy    442 tggagtgtgtgccttgtggagaccctcctcctccttacgaaccgcactgtgccagcaagg 501
          |||||||||||||| || |||||||| |||||||| |||||||| |||||| |||||||||
Db    524 TGGAGTGTGTGCCCTGCGGAGACCCACCTCCTCCCTACGAACCACACTGTACCAGCAAGG 583

Qy    502 tcaacctcgtgaagatcgcgtccacggcctccagcccacgggacacggcgctggctgccg 561
          | ||||| |||||||||| | ||||| | |||||||||| ||||||||||||||||||||
Db    584 TGAACCTTGTGAAGATCTCCTCCACCGTCTCCAGCCCTCGGGACACGGCGCTGGCTGCCG 643

Qy    562 ttatctgcagcgctctggccaccgtcctgctggccctgctcatcctctgtgtcatctatt 621
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Db    644 TCATCTGCAGTGCTCTGGCCACGGTGCTGCTCGCCCTGCTCATCCTGTGTGTCATCTACT 703

Qy    622 gtaagagacagtttatggagaagaaacccagctggtctctgcggtcacaggacattcagt 681
          | ||||| |||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    704 GCAAGAGGCAGTTCATGGAGAAGAAACCCAGCTGGTCTCTGCGGTCACAGGACATTCAGT 763

Qy    682 acaacggctctgagctgtcgtgtcttgacagacctcagctccacgaatatgcccacagag 741
          |||| ||||||||||||| ||  |||||    |||| ||||| | | | |||||| ||||
Db    764 ACAATGGCTCTGAGCTGTCATGCTTTGACCAGCCTCGGCTCCGCCACTGTGCCCATAGAG 823

Qy    742 cctgctgccagtgccgccgtgactcagtgcagacctgcgggccggtgcgcttgctcccat 801
          | ||||| |||| | ||| |||||||  |  |  |  ||||| || | | || | || |
Db    824 CATGCTGTCAGTATCACCGGGACTCAGCCCCAATGTATGGGCCTGTTCACCTGATTCCGT 883

Qy    802 ccatgtgctgtgaggaggcctgcagccccaacccggcgactcttggttgtggggtgcatt 861
          || |||||||||| |||||| ||||| |   ||  ||    ||||| |||||| ||| ||
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Db     884 CCTTGTGCTGTGAAGAGGCCCGCAGCTCTGCCCGAGCTGTGCTTGGCTGTGGGCTGCGTT 943

Qy     862 ctgcagccagtcttcaggcaagaaacgcaggcccagccgggggagatggtgccgactttct 921
           || |  | |  || ||||  |||||| | |    | |  ||||| | | ||||  | ||||
Db     944 CTCCCACTACCCTCCAGGAGAGAAACCCGGCTTCTGTGGGGGACACGATGCCAGCCTTCT 1003

Qy     922 tcggatccctcacgcagtccatctgtggcgagttttcagatgcctggcctctgatgcaga 981
           ||||  ||  |  | |  ||||||||  |  || ||||| ||||||||||||||||||||
Db    1004 TCGGGTCTGTTTCCCGTTCCATCTGCGCTGAATTTTCTGATGCCTGGCCTCTGATGCAGA 1063

Qy     982 atcccatgggtggtgacaacatctctttttgtgactcttatcctgaactcactggagaag 1041
           ||||  |||||||||    ||| |||| | ||||||||||||||||||||||||||||||
Db    1064 ATCCTCTGGGTGGTG---ACAGCTCTCTCTGTGACTCTTATCCTGAACTCACTGGAGAAG 1120

Qy    1042 acattcattctctcaatccagaacttgaaagctcaacgtctttggattcaaatagcagtc 1101
           | |   |||| |||||||| |||   |||||| || | ||| |||||||  | | || | |
Db    1121 ATACCAATTCCCTCAATCCCGAAAACGAAAGCGCAGCATCTCTGGATTCCAGTGGCGGCC 1180

Qy    1102 aagatttggttggtggggctgttccagtccagtctcattctgaaaactttacagcagcta 1161
           | ||| ||| |||    |||| || ||     |||     ||          |  | |
Db    1181 AGGATCTGGCTGGGACAGCTGCTCTAGAGTCTTCTGGGAATGTTTCAGAATCTACTGACT 1240

Qy    1162 ctgatttatctagatataacaacacactggtagaatcagcatcaactcaggatgcactaa 1221
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Db    1241 CACCTAGACATGGTGACACTGGTACAGTCTGGGAGCAGACGCTAGCTCAGGATGCTCAAA 1300

Qy    1222 ctatgagaagccagctagatcaggagagtggcgctatcatccacccagccactcagacgt 1281
             |  ||||||   ||    |||     | |  | | |  | | |||||  |  ||
Db    1301 GGACTCCAAGCCAAGGAGGCTGGGAAGACAGGGAAAACCTGAATCTAGCCATGCCCACAG 1360

Qy    1282 ccctccagg 1290
           || |||||||
Db    1361 CCTTCCAGG 1369


RESULT   4
AF167552
LOCUS       AF167552     1678 bp    mRNA            ROD       25-MAY-2000
DEFINITION  Mus musculus TAJ-alpha long mRNA, complete cds.
ACCESSION   AF167552
VERSION     AF167552.1  GI:8071637
KEYWORDS    .
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1678)
  AUTHORS   Eby,M.T., Jasmin,A., Kumar,A., Sharma,K. and Chaudhary,P.M.
  TITLE     TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
            Activates the c-Jun N-terminal Kinase Pathway and Mediates
            Caspase-independent Cell Death
  JOURNAL   J. Biol. Chem. 275 (20), 15336-15342 (2000)
   PUBMED   10809768
REFERENCE   2  (bases 1 to 1678)
  AUTHORS   Chaudhary,P.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-JUL-1999) Internal Medicine, UT Southwestern Medical
            Center, 5323 Harry Hines Blvd., Dallas, TX 75235-8593, USA
FEATURES             Location/Qualifiers
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                     SLNPENESTASLDSSGGQDLAGTAALESSGNVSESTDSPRHGDTGTVWEQTLAQDAQR
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BASE COUNT      371 a    467 c    466 g    374 t
ORIGIN


  Query Match             49.5%;  Score 741;  DB 11;  Length 1678;
  Best Local Similarity   74.5%;  Pred. No. 7e-145;
  Matches  946;  Conservative    0;  Mismatches  320;  Indels    3;  Gaps    1;

Qy      22 aataaatacatttgataagaaagatggctttaaaagtgctactagaacaagagaaaacgt 81
           |||||| || |||| | |||   |||||  | || || ||||    |||   ||    |
Db      49 AATAAACACGTTTGGTGAGAGCCATGGCACTCAAGGTCCTACCTCTACACAGGACGGTGC 108

Qy      82 ttttcactcttttagtattactaggctatttgtcatgtaaagtgacttgtgaaacaggag 141
           | ||| ||    |  | || |||  | |  || ||||||||||||| ||| |||||  ||||
Db     109 TCTTCGCTGCCATTCTCTTCCTACTCCACCTGGCATGTAAAGTGAGTTGCGAAACCGGAG 168

Qy     142 actgtagacagcaagaattcagggatcggtctggaaactgtgttccctgcaaccagtgtg 201
           | || || ||||| ||||||| |||||| |||||||||||||||| | |||||| |||||
Db     169 ATTGCAGGCAGCAGGAATTCAAGGATCGATCTGGAAACTGTGTCCTCTGCAAACAGTGCG 228

Qy     202 ggccaggcatggagttgtctaaggaatgtggcttcggctatggggaggatgcacagtgtg 261
           | || |||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db     229 GACCTGGCATGGAGTTGTCCAAGGAATGTGGCTTCGGCTATGGGGAGGATGCACAGTGTG 288

Qy     262 tgacgtgccggctgcacaggttcaaggaggactggggcttccagaaatgcaagccctgtc 321
           || | ||| ||| |||| |||||||||| |||||||| |||||||| || ||||| |||
Db     289 TGCCCTGCAGGCCGCACCGGTTCAAGGAAGACTGGGGTTTCCAGAAGTGTAAGCCATGTG 348

Qy     322 tggactgcgcagtggtgaaccgctttcagaaggcaaattgttcagccaccagtgatgcca 381
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Db     349 CGGACTGTGCGCTGGTGAACCGCTTTCAGAGGGCCAACTGCTCACACACCAGTGATGCTG 408

Qy     382 tctgcggggactgcttgccaggattttataggaagacgaaacttgtcggctttcaagaca 441
           |||||||||||||| ||||||||||||  ||||||| ||||| || || ||||||||||
Db     409 TCTGCGGGGACTGCCTGCCAGGATTTTACCGGAAGACCAAACTGGTTGGTTTTCAAGACA 468

Qy     442 tggagtgtgtgccttgtggagaccctcctcctcctcttacgaaccgcactgtgccagcaagg 501
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Db     469 TGGAGTGTGTGCCCTGCGGAGACCCACCTCCTCCCTACGAACCACACTGTACCAGCAAGG 528

Qy     502 tcaacctcgtgaagatcgcgtccacggcctccagcccacgggacacggcgctggctgccg 561
           | ||||| |||||||||| | ||||| | |||||||||| ||||||||||||||||||||
Db     529 TGAACCTTGTGAAGATCTCCTCCACCGTCTCCAGCCCTCGGGACACGGCGCTGGCTGCCG 588

Qy     562 ttatctgcagcgctctggccaccgtcctgctggccctgctcatcctctgtgtcatctatt 621
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Db     589 TCATCTGCAGTGCTCTGGCCACGGTGCTGCTCGCCCTGCTCATCCTGTGTGTCATCTACT 648

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Db     649 GCAAGAGGCAGTTCATGGAGAAGAAACCCAGCTGGTCTCTGCGGTCACAGGACATTCAGT 708

Qy     682 acaacggctctgagctgtcgtgtcttgacagacctcagctccacgaatatgcccacagag 741
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Db     709 ACAATGGCTCTGAGCTGTCATGCTTTGACCAGCCTCGGCTCCGCCACTGTGCCCATAGAG 768

Qy     742 cctgctgccagtgccgccgtgactcagtgcagacctgcgggccggtgcgcttgctcccat 801
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Qy     802 ccatgtgctgtgaggaggcctgcagccccaacccggcgactcttggttgtggggtgcatt 861
           || |||||||||| |||||| ||||| |   ||  ||    ||||| |||||| ||| ||
Db     829 CCTTGTGCTGTGAAGAGGCCCGCAGCTCTGCCCGAGCTGTGCTTGGCTGTGGGCTGCGTT 888

Qy     862 ctgcagccagtcttcaggcaagaaacgcaggcccagccgggggagatggtgccgactttct 921
           || |  | |  || ||||  |||||| | |.  | |  ||| | | | ||||  | ||||
Db     889 CTCCCACTACCCTCCAGGAGAGAAACCCGGCTTCTGTGGGGAACACGATGCCAGCCTTCT 948

Qy     922 tcggatccctcacgcagtccatctgtggcgagttttcagatgcctggcctctgatgcaga 981
           | || ||  |  | |  ||||||||  |  |||||||| ||||||||||||||||||||
Db     949 TTGGGTCTGTTTCCCGTTCCATCTGCGCGGAGTTTTCTGATGCCTGGCCTCTGATGCAGA 1008
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Qy    982 atcccatgggtggtgacaacatctcttttgtgactcttatcctgaactcactggagaag 1041
          ||||  |||| ||||   ||| |||| | ||||||||||||||||||||||||||||||
Db   1009 ATCCTCTGGGCGGTG---ACAGCTCTCTCTGTGACTCTTATCCTGAACTCACTGGAGAAG 1065

Qy   1042 acattcattctctcaatccagaacttgaaagctcaacgtctttggattcaaatagcagtc 1101
          | |   |||| |||||||| |||   |||||| || | ||| ||||||| | | || | |
Db   1066 ATACCAATTCCCTCAATCCCGAAAACGAAAGCACAGCATCTCTGGATTCCAGTGGCGGCC 1125

Qy   1102 aagatttggttggtggggctgttccagtccagtctcattctgaaaactttacagcagcta 1161
          | ||| ||| |||    |||| || ||     |||     ||         |  | |
Db   1126 AGGATCTGGCTGGGACAGCTGCTCTAGAGTCTTCTGGGAATGTTTCAGAATCTACTGACT 1185

Qy   1162 ctgatttatctagatataacaacacactggtagaatcagcatcaactcaggatgcactaa 1221
          |  |  |  | |  | |     ||| |    ||     |   | ||||||||| | ||
Db   1186 CACCTAGACATGGTGACACTGGTACAGTCTGGGAGCAGACGCTAGCTCAGGATGCTCAAA 1245

Qy   1222 ctatgagaagccagctagatcaggagagtggcgctatcatccacccagccactcagacgt 1281
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Db   1246 GGACTCCAAGCCAAGGAGGCTGGGAAGACAGGGAAAACCTGAATCTAGCCATGCCCACAG 1305

Qy   1282 ccctccagg 1290
          || ||||||
Db   1306 CCTTCCAGG 1314
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RESULT   5
AF173166
LOCUS       AF173166     1075 bp    mRNA            ROD       26-DEC-1999
DEFINITION  Mus musculus TNFRSF19 mRNA, complete cds.
ACCESSION   AF173166
VERSION     AF173166.1  GI:6635354
KEYWORDS    .
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1075)
  AUTHORS   Hu,S., Tamada,K., Ni,J., Vincenz,C. and Chen,L.
  TITLE     Characterization of TNFRSF19, a novel member of the tumor necrosis
            factor receptor superfamily
  JOURNAL   Genomics 62 (1), 103-107 (1999)
  MEDLINE   20054362
REFERENCE   2  (bases 1 to 1075)
  AUTHORS   Hu,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-JUL-1999) Department of Immunology, Mayo Clinic and
            Foundation, 200 First Street SW, Rochester, MN 55905, USA
FEATURES             Location/Qualifiers
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BASE COUNT      211 a    308 c    296 g    259 t      1 others
ORIGIN
```

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  Query Match             46.3%;  Score 692.6;  DB 11;  Length 1075;
  Best Local Similarity   78.7%;  Pred. No. 8.9e-135;
  Matches  840;  Conservative    0;  Mismatches  224;  Indels    3;  Gaps    1;

Qy     22 aataaatacatttgataagaaagatggctttaaaagtgctactagaacaagagaaaacgt 81
          |||||| || |||| | |||   |||||  | || || ||||    |||   ||    |
Db      5 AATAAACACGTTTGGTGAGAGCCATGGCACTCAAGGTCCTACCTCTACACAGGACGGTGC 64

Qy     82 ttttcactcttttagtattactaggctatttgtcatgtaaagtgacttgtgaaacaggag 141
          | ||| ||     |  | || |||  | |  || |||||||||||| ||| ||| | ||||
Db     65 TCTTCGCTGCCATTCTCTTCCTACTCCACCTGGCATGTAAAGTGAGTTGCGAAGCCGGAG 124

Qy    142 actgtagacagcaagaattcagggatcggtctggaaactgtgttccctgcaaccagtgtg 201
          | || || ||||| ||||||| ||||||| |||||||||||||| | |||||| ||||| |
Db    125 ATTGCAGGCAGCAGGAATTCAAGGATCGATCTGGAAACTGTGTCCTCTGCAAACAGTGCG 184

Qy    202 ggccaggcatggagttgtctaaggaatgtggcttcggctatggggaggatgcacagtgtg 261
          | || |||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    185 GACCTGGCATGGAGTTGTCCAAGGAATGTGGCTTCGGCTATGGGGAGGATGCACAGTGTG 244

Qy    262 tgacgtgccggctgcacaggttcaaggaggactggggcttccagaaatgcaagccctgtc 321
          || | ||| ||| |||| |||||||||| |||||||| |||||||| || ||||| |||
Db    245 TGCCCTGCAGGCCGCACCGGTTCAAGGAAGACTGGGGTTTCCAGAAGTGTAAGCCATGTG 304

Qy    322 tggactgcgcagtggtgaaccgctttcagaaggcaaattgttcagccaccagtgatgcca 381
          ||||||  ||  |||||||||||||||||| ||| || || |||  ||||||||||||
Db    305 CGGACTGTGCGCTGGTGAACCGCTTTCAGAGGGCCAACTGCTCACACACCAGTGATGCTG 364

Qy    382 tctgcggggactgcttgccaggattttataggaagacgaaacttgtcggctttcaagaca 441
          |||||||||||||| ||||||||||||  ||||||| ||||| || || ||||||||||
Db    365 TCTGCGGGGACTGCCTGCCAGGATTTTACCGGAAGACCAAACTGGTTGGTTTTCAAGACA 424

Qy    442 tggagtgtgtgccttgtggagaccctcctcctccttacgaaccgcactgtgccagcaagg 501
          |||||||||||| || |||||||| |||||||| |||||| ||||||| |||||||||
Db    425 TGGAGTGTGTGCCCTGCGGAGACCCACCTCCTCCCTACGAACCACACTGTACCAGCAAGG 484

Qy    502 tcaacctcgtgaagatcgcgtccacggcctccagcccacgggacacggcgctggctgccg 561
          | ||||| |||||||||  | ||||| | |||||||| ||||||||||||||||||||||
Db    485 TGAACCTTGTGAAGATCTCCTCCACCGTCTCCAGCCCTCGGGACACGGCGCTGGCTGCCG 544

Qy    562 ttatctgcagcgctctggccaccgtcctgctggccctgctcatcctctgtgtcatctatt 621
          | |||||||| |||||||||||  || ||||| |||||||||||||| ||||||||||| |
Db    545 TCATCTGCAGTGCTCTGGCCACGGTGCTGCTCGCCCTGCTCATCCTGTGTGTCATCTACT 604

Qy    622 gtaagagacagtttatggagaagaaaacccagctggtctctgcggtcacaggacattcagt 681
          | ||||| |||| |||||||||||||||||||||||||||||||||| ||||||||||||||
Db    605 GCAAGAGGCAGTTCATGGAGAAGAAACCCAGCTGGTCTCTGCGGCCACAGGACATTCAGT 664

Qy    682 acaacggctctgagctgtcgtgtcttgacagacctcagctccacgaatatgcccacagag 741
          |||| |||||||||||||| ||  |||||   |||| ||||| | | | |||||| ||||
Db    665 ACAATGGCTCTGAGCTGTCATGCTTTGACCAGCCTCGGCTCCGCCACTGTGCCCATAGAG 724

Qy    742 cctgctgccagtgccgccgtgactcagtgcagacctgcgggccggtgcgcttgctcccat 801
          | ||||| |||| | ||| ||||||| |  |  |  ||||| || | | || | || |
Db    725 CATGCTGTCAGTATCACCGGGACTCAGCCCCAATGTATGGGCCTGTTCACCTGATTCCGT 784

Qy    802 ccatgtgctgtgaggaggcctgcagccccaacccggcgactcttggttgtggggtgcatt 861
          || |||||||||| |||||| ||||| |   ||  ||   ||||| |||||| ||| ||
Db    785 CCTTGTGCTGTGAAGAGGCCCGCAGCTCTGCCCGAGCTGTGCTTGGCTGTGGGCTGCGTT 844

Qy    862 ctgcagccagtcttcaggcaagaaacgcaggcccagccggggagatggtgccgacttttct 921
          || |  | |  || ||||  |||||| | |   | |  ||| | | | ||||  | ||||
Db    845 CTCCCACTACCCTCCAGGAGAGAAACCCGGCTTCTGTGGGGAACACGATGCCAGCCTTCT 904

Qy    922 tcggatccctcacgcagtccatctgtggcgagttttcagatgcctggcctctgatgcaga 981
          | || ||  |  | |  |||||||| |  |||||||| ||||||||||||||||||||||
Db    905 TTGGGTCTGTTTCCCGTTCCATCTGCGCGGAGTTTTCTGATGCCTGGCCTCTGATGCAGA 964

Qy    982 atcccatgggtggtgacaacatctcttttgtgactcttatcctgaactcactggagaag 1041
          ||||  |||| ||||   ||| |||| | ||||||||||||||||||||||||||||||
Db    965 ATCCTCTGGGCGGTG---ACAGCTCTCTCTGTGACTCTTATCCTGAACTCACTGGAGAAG 1021

Qy   1042 acattcattctctcaatccagaacttgaaagctcaacgtctttggat 1088
          | |   |||| ||||||||||  |    |||     | |  ||||
Db   1022 ATACCAATTCCCTCAATCCAGAGATGCTGTGCTTTCGTTTTCGGGAT 1068
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RESULT   6
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```
AL161422
LOCUS       AL161422   143608 bp    DNA             HTG       20-SEP-2000
DEFINITION  Homo sapiens chromosome 13 clone RP11-168G12, *** SEQUENCING IN
            PROGRESS ***, 3 unordered pieces.
ACCESSION   AL161422
VERSION     AL161422.13  GI:10277928
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 143608)
  AUTHORS   Pearce,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
            requests: clonerequest@sanger.ac.uk
COMMENT     On Sep 22, 2000 this sequence version replaced gi:10190601.
            -------------- Genome Center
            Center: Sanger Centre
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            -------------- Project Information
            Center project name: bA168G12
            -------------- Summary Statistics
            Assembly program: XGAP4; version 4.5
            Sequencing vector: plasmid; L08752; 100% of reads
            Chemistry: Dye-terminator Big Dye; 100% of reads
            Consensus quality: 143007 bases at least Q40
            Consensus quality: 143260 bases at least Q30
            Consensus quality: 143347 bases at least Q20
            Insert size: 143408; sum-of-contigs
            Insert size: 145175; 5.9% error; agarose-fp
            Quality coverage: 8.55x in Q20 bases; sum-of-contigs Quality
            coverage: 8.58x in Q20 bases; agarose-fp
            --------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 3 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     2992: contig of 2992 bp in length
            *     2993 3092: gap of      100 bp
            *     3093   129375: contig of 126283 bp in length
            *   129376 129475: gap of      100 bp
            *   129476   143608: contig of 14133 bp in length.
FEATURES             Location/Qualifiers
     source          1. .143608
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="13"
                     /clone="RP11-168G12"
                     /clone_lib="RPCI-11.1"
     misc_feature    1. .2992
                     /note="assembly_fragment:01799
                     fragment_chain:1"
     misc_feature    3093. .129375
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                     fragment_chain:1
                     clone_end:T7
                     vector_side:left"
     misc_feature    129476. .143608
                     /note="assembly_fragment:00106"
BASE COUNT    41121 a  29506 c  30419 g  42362 t    200 others
ORIGIN


  Query Match            39.2%;  Score 586.6;  DB 73;  Length 143608;
  Best Local Similarity  97.7%;  Pred. No. 1.8e-112;
  Matches  595;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy     882 agaaacgcaggcccagccggggagatggtgccgactttcttcggatccctcacgcagtcc 941
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   84813 AGAAACGCAGGCCCAGCCGGGGAGATGGTGCCGACTTTCTTCGGATCCCTCACGCAGTCC 84872

Qy     942 atctgtggcgagttttcagatgcctggcctctgatgcagaatcccatgggtggtgacaac 1001
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   84873 ATCTGTGGCGAGTTTTCAGATGCCTGGCCTCTGATGCAGAATCCCATGGGTGGTGACAAC 84932

Qy    1002 atctctttttgtgactcttatcctgaactcactggagaagacattcattctctcaatcca 1061
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   84933 ATCTCTTTTTGTGACTCTTATCCTGAACTCACTGGAGAAGACATTCATTCTCTCAATCCA 84992

Qy    1062 gaacttgaaagctcaacgtctttggattcaaatagcagtcaagatttggttggtggggct 1121
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   84993 GAACTTGAAAGCTCAACGTCTTTGGATTCAAATAGCAGTCAAGATTTGGTTGGTGGGGCT 85052

Qy    1122 gttccagtccagtctcattctgaaaactttacagcagctactgatttatctagatataac 1181
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   85053 GTTCCAGTCCAGTCTCATTCTGAAAACTTTACAGCAGCTACTGATTTATCTAGATATAAC 85112

Qy    1182 aacacactggtagaatcagcatcaactcaggatgcactaactatgagaagccagctagat 1241
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   85113 AACACACTGGTAGAATCAGCATCAACTCAGGATGCACTAACTATGAGAAGCCAGCTAGAT 85172

Qy    1242 caggagagtggcgctatcatccacccagccactcagacgtccctccaggtaaggcagcga 1301
           |||||||||||  ||| ||||||||||||||||||||||||||||||||||||||||||||
Db   85173 CAGGAGAGTGGTGCTGTCATCCACCCAGCCACTCAGACGTCCCTCCAGGTAAGGCAGCGA 85232

Qy    1302 ctgggttccctgtgaacacagcactgacttacagtagatcagaactctgttcccagcata 1361
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   85233 CTGGGTTCCCTGTGAACACAGCACTGACTTACAGTAGATCAGAACTCTGTTCCCAGCATA 85292

Qy    1362 agatttgggggaacctgatgagttttttttttgcatctttaataatttcttgtatgttgt 1421
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   85293 AGATTTGGGGGAACCTGATGAGTTTTTTTTTTGCATCTTTAATAATTTCTTGTATGTTGT 85352

Qy    1422 agagtatgttttaaaataaatttcaagtatttttttttaaaaactaaaaaaaaaaaaaaaa 1481
           |||||||||||||||||||||||||||||||||| ||||||||| | |    || | |
Db   85353 AGAGTATGTTTTAAAATAAATTTCAAGTATTTTTTTAAAAAACTAACACAGCTAATATAT 85412

Qy    1482 aaaaaaaaa 1490
           || |  |||
Db   85413 AAGAGCAAA 85421


RESULT   7
AL139080
LOCUS       AL139080   178256 bp    DNA             HTG       29-SEP-2000
DEFINITION  Homo sapiens chromosome 13 clone RP11-173N17 map q12.11-12.3, ***
            SEQUENCING IN PROGRESS ***, 15 unordered pieces.
ACCESSION   AL139080
VERSION     AL139080.8  GI:10443032
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 178256)
  AUTHORS   Burton,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
            requests: clonerequest@sanger.ac.uk
COMMENT     On Oct 1, 2000 this sequence version replaced gi:10129398.
            -------------- Genome Center
            Center: Sanger Centre
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            -------------- Project Information
            Center project name: bA173N17
```

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            ------------- Summary Statistics
            Assembly program: XGAP4; version 4.5
            Sequencing vector: plasmid; L08752; 100% of reads
            Chemistry: Dye-terminator Big Dye; 100% of reads
            Consensus quality: 168976 bases at least Q40
            Consensus quality: 172107 bases at least Q30
            Consensus quality: 173780 bases at least Q20
            Insert size: 176856; sum-of-contigs
            Insert size: 163577; 8.6% error; agarose-fp
            Quality coverage: 3.73x in Q20 bases; sum-of-contigs Quality
            coverage: 4.07x in Q20 bases; agarose-fp
            -------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 15 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     8223: contig of 8223 bp in length
            *     8224  8323: gap of      100 bp
            *     8324    25426: contig of 17103 bp in length
            *    25427  25526: gap of      100 bp
            *    25527    28263: contig of 2737 bp in length
            *    28264  28363: gap of      100 bp
            *    28364    34273: contig of 5910 bp in length
            *    34274  34373: gap of      100 bp
            *    34374    42235: contig of 7862 bp in length
            *    42236  42335: gap of      100 bp
            *    42336    53917: contig of 11582 bp in length
            *    53918  54017: gap of      100 bp
            *    54018    71972: contig of 17955 bp in length
            *    71973  72072: gap of      100 bp
            *    72073    81711: contig of 9639 bp in length
            *    81712  81811: gap of      100 bp
            *    81812    88644: contig of 6833 bp in length
            *    88645  88744: gap of      100 bp
            *    88745    95048: contig of 6304 bp in length
            *    95049  95148: gap of      100 bp
            *    95149   107455: contig of 12307 bp in length
            *   107456 107555: gap of      100 bp
            *   107556   125465: contig of 17910 bp in length
            *   125466 125565: gap of      100 bp
            *   125566   140008: contig of 14443 bp in length
            *   140009 140108: gap of      100 bp
            *   140109   144761: contig of 4653 bp in length
            *   144762 144861: gap of      100 bp
            *   144862   178256: contig of 33395 bp in length.
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                     /db_xref="taxon:9606"
                     /chromosome="13"
                     /map="q12.11-12.3"
                     /clone="RP11-173N17"
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     misc_feature    1. .8223
                     /note="assembly_fragment:01724
                     fragment_chain:1"
     misc_feature    8324. .25426
                     /note="assembly_fragment:00074
                     fragment_chain:1"
     misc_feature    25527. .28263
                     /note="assembly_fragment:01884
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     misc_feature    28364. .34273
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     misc_feature    34374. .42235
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     misc_feature    42336. .53917
                     /note="assembly_fragment:00364
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     misc_feature    54018. .71972
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     misc_feature    81812. .88644
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     misc_feature    88745. .95048
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     misc_feature    95149. .107455
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     misc_feature    125566. .140008
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                     /note="assembly_fragment:01533
                     fragment_chain:5"
     misc_feature    144862. .178256
                     /note="assembly_fragment:01008"
BASE COUNT    52999 a  37393 c  36460 g  49998 t   1406 others
ORIGIN


  Query Match             39.2%;  Score 586.6;  DB 72;  Length 178256;
  Best Local Similarity   97.7%;  Pred. No. 1.8e-112;
  Matches  595;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy     882 agaaacgcaggcccagccggggagatggtgccgactttcttcggatccctcacgcagtcc 941
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46631 AGAAACGCAGGCCCAGCCGGGGAGATGGTGCCGACTTTCTTCGGATCCCTCACGCAGTCC 46690

Qy     942 atctgtggcgagttttcagatgcctggcctctgatgcagaatcccatgggtggtgacaac 1001
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46691 ATCTGTGGCGAGTTTTCAGATGCCTGGCCTCTGATGCAGAATCCCATGGGTGGTGACAAC 46750

Qy    1002 atctcttttttgtgactcttatcctgaactcactggagaagacattcattctctcaatcca 1061
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46751 ATCTCTTTTTGTGACTCTTATCCTGAACTCACTGGAGAAGACATTCATTCTCTCAATCCA 46810

Qy    1062 gaacttgaaagctcaacgtctttggattcaaatagcagtcaagatttggttggtggggct 1121
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46811 GAACTTGAAAGCTCAACGTCTTTGGATTCAAATAGCAGTCAAGATTTGGTTGGTGGGGCT 46870

Qy    1122 gttccagtccagtctcattctgaaaactttacagcagctactgatttatctagatataac 1181
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46871 GTTCCAGTCCAGTCTCATTCTGAAAACTTTACAGCAGCTACTGATTTATCTAGATATAAC 46930

Qy    1182 aacacactggtagaatcagcatcaactcaggatgcactaactatgagaagccagctagat 1241
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46931 AACACACTGGTAGAATCAGCATCAACTCAGGATGCACTAACTATGAGAAGCCAGCTAGAT 46990

Qy    1242 caggagagtggcgctatcatccacccagccactcagacgtccctccaggtaaggcagcga 1301
           |||||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||
Db   46991 CAGGAGAGTGGTGCTGTCATCCACCCAGCCACTCAGACGTCCCTCCAGGTAAGGCAGCGA 47050

Qy    1302 ctgggttccctgtgaacacagcactgacttacagtagatcagaactctgttcccagcata 1361
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   47051 CTGGGTTCCCTGTGAACACAGCACTGACTTACAGTAGATCAGAACTCTGTTCCCAGCATA 47110

Qy    1362 agatttgggggaacctgatgagttttttttttgcatctttaataatttcttgtatgttgt 1421
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   47111 AGATTTGGGGGAACCTGATGAGTTTTTTTTTTGCATCTTTAATAATTTCTTGTATGTTGT 47170

Qy    1422 agagtatgttttaaaataaatttcaagtatttttttttaaaaactaaaaaaaaaaaaaaaa 1481
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          |||||||||||||||||||||||||||||||||||| |||||||| | |   || | |
Db  47171 AGAGTATGTTTTAAAATAAATTTCAAGTATTTTTTTAAAAAACTAACACAGCTAATATAT 47230

Qy   1482 aaaaaaaaa 1490
          || |  |||
Db  47231 AAGAGCAAA 47239


RESULT   8
AB040433
LOCUS       AB040433      744 bp    mRNA            ROD       22-JUL-2000
DEFINITION  Mus musculus mRNA for dTROY, complete cds.
ACCESSION   AB040433
VERSION     AB040433.1  GI:9392327
KEYWORDS    dTROY.
SOURCE      Mus musculus cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (sites)
  AUTHORS   Kojima,T., Morikawa,Y., Copeland,N.G., Gilbert,D.J., Jenkins,N.A.,
            Senba,E. and Kitamura,T.
  TITLE     TROY, a newly identified member of the tumor necrosis factor
            receptor superfamily, exhibits a homology with Edar and is
            expressed in embryonic skin and hair follicles
  JOURNAL   J. Biol. Chem. 275 (27), 20742-20747 (2000)
  MEDLINE   20347167
REFERENCE   2  (bases 1 to 744)
  AUTHORS   Kojima,T. and Kitamura,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-MAR-2000) to the DDBJ/EMBL/GenBank databases. Tetsuo
            Kojima, Chugai Research Institute for Molecular Medicine, Inc.,
            Cytokine Research Program; 153-2 Nagai, Niihari, Ibaraki 300-4101,
            Japan (E-mail:kojimat@cimmed.com, Tel:81-298-306211,
            Fax:81-298-306270)
FEATURES             Location/Qualifiers
     source          1. .744
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                     /db_xref="taxon:10090"
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     CDS             67. .711
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                     /note="a member of TNFR superfamily exhibits a homology
                     with Edar"
                     /codon_start=1
                     /product="dTROY"
                     /protein_id="BAB03268.1"
                     /db_xref="GI:9392328"
                     /translation="MALKVLPLHRTVLFAAILFLLHLACKVSCETGDCRQQEFKDRSG
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                     RANCSHTSDAVCGDCLPGFYRKTKLVGFQDMECVPCGDPPPPYEPHCTSKVNLVKISS
                     TVSSPRDTALAAVICSALATVLLALLILCVIYCKRQFMEKKPSCKLPSLCLTVK"
BASE COUNT      162 a    208 c    211 g    163 t
ORIGIN


  Query Match           30.8%;  Score 460.8;  DB 11;  Length 744;
  Best Local Similarity  81.9%;  Pred. No. 2.5e-86;
  Matches  531;  Conservative    0;  Mismatches  117;  Indels    0;  Gaps    0;

Qy      22 aataaatacatttgataagaaagatggctttaaaagtgctactagaacaagagaaaacgt 81
           |||||| || |||| | |||   |||||  | || || ||||    |||   ||    |
Db      44 AATAAACACGTTTGGTGAGAGCCATGGCACTCAAGGTCCTACCTCTACACAGGACGGTGC 103

Qy      82 ttttcactcttttagtattactaggctatttgtcatgtaaagtgacttgtgaaacaggag 141
           | ||| ||    |  | || |||  | |  || ||||||||||| ||| ||||| ||||
Db     104 TCTTCGCTGCCATTCTCTTCCTACTCCACCTGGCATGTAAAGTGAGTTGCGAAACCGGAG 163

Qy     142 actgtagacagcaagaattcagggatcggtctggaaactgtgttccctgcaaccagtgtg 201
           | || || ||||| ||||||| |||||| |||||||||||||| | |||||| ||||| |
Db     164 ATTGCAGGCAGCAGGAATTCAAGGATCGATCTGGAAACTGTGTCCTCTGCAAACAGTGCG 223

Qy     202 ggccaggcatggagttgtctaaggaatgtggcttcggctatggggaggatgcacagtgtg 261
           | || |||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db     224 GACCTGGCATGGAGTTGTCCAAGGAATGTGGCTTCGGCTATGGGGAGGATGCACAGTGTG 283

Qy     262 tgacgtgccggctgcacaggttcaaggaggactggggcttccagaaatgcaagccctgtc 321
           || | ||| ||| |||| |||||||||| |||||||| |||||||| || ||||| |||
Db     284 TGCCCTGCAGGCCGCACCGGTTCAAGGAAGACTGGGGTTTCCAGAAGTGTAAGCCATGTG 343

Qy     322 tggactgcgcagtggtgaaccgctttcagaaggcaaattgttcagccaccagtgatgcca 381
           ||||||  ||  |||||||||||||||||| ||| || || |||  ||||||||||||
Db     344 CGGACTGTGCGCTGGTGAACCGCTTTCAGAGGGCCAACTGCTCACACACCAGTGATGCTG 403

Qy     382 tctgcggggactgcttgccaggattttataggaagacgaaacttgtcggctttcaagaca 441
           |||||||||||||| ||||||||||||  ||||||| ||||| || || ||||||||||
Db     404 TCTGCGGGGACTGCCTGCCAGGATTTTACCGGAAGACCAAACTGGTTGGTTTTCAAGACA 463

Qy     442 tggagtgtgtgccttgtggagaccctcctcctcctcttacgaaccgcactgtgccagcaagg 501
           |||||||||||||| || |||||||| |||||||| |||||||| |||||| |||||||||
Db     464 TGGAGTGTGTGCCCTGCGGAGACCCACCTCCTCCCTACGAACCACACTGTACCAGCAAGG 523

Qy     502 tcaacctcgtgaagatcgcgtccacggcctccagcccacgggacacggcgctggctgccg 561
           | ||||| ||||||||| | ||||| | |||||||| ||||||||||||||||||||||
Db     524 TGAACCTTGTGAAGATCTCCTCCACCGTCTCCAGCCCTCGGGACACGGCGCTGGCTGCCG 583

Qy     562 ttatctgcagcgctctggccaccgtcctgctggccctgctcatcctctgtgtcatctatt 621
           | |||||||| |||||||||| || ||||| |||||||||||||| |||||||||| |
Db     584 TCATCTGCAGTGCTCTGGCCACGGTGCTGCTCGCCCTGCTCATCCTGTGTGTCATCTACT 643

Qy     622 gtaagagacagtttatggagaagaaacccagctggtctctgcggtcac 669
           | ||||| ||||| ||||||||||||||||||||    || |  || |
Db     644 GCAAGAGGCAGTTCATGGAGAAGAAACCCAGCTGTAAGCTCCCATCCC 691


RESULT   9
AF167553
LOCUS       AF167553      886 bp    mRNA            ROD       25-MAY-2000
DEFINITION  Mus musculus TAJ-alpha short mRNA, complete cds.
ACCESSION   AF167553
VERSION     AF167553.1  GI:8071639
KEYWORDS    .
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 886)
  AUTHORS   Eby,M.T., Jasmin,A., Kumar,A., Sharma,K. and Chaudhary,P.M.
  TITLE     TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
            Activates the c-Jun N-terminal Kinase Pathway and Mediates
            Caspase-independent Cell Death
  JOURNAL   J. Biol. Chem. 275 (20), 15336-15342 (2000)
   PUBMED   10809768
REFERENCE   2  (bases 1 to 886)
  AUTHORS   Chaudhary,P.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-JUL-1999) Internal Medicine, UT Southwestern Medical
            Center, 5323 Harry Hines Blvd., Dallas, TX 75235-8593, USA
FEATURES             Location/Qualifiers
     source          1. .886
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone_lib="Soares p3NMF19.5"
     CDS             72. .716
                     /note="decoy receptor"
                     /codon_start=1
                     /product="TAJ-alpha short"
                     /protein_id="AAF71826.1"
                     /db_xref="GI:8071640"
                     /translation="MALKVLPLHRTVLFAAILFLLHLACKVSCETGDCRQQEFKDRSG
                     NCVLCKQCGPGMELSKECGFGYGEDAQCVPCRPHRFKEDWGFQKCKPCADCALVNRFQ
                     RANCSHTSDAVCGDCLPGFYRKTKLVGFQDMECVPCGDPPPPYEPHCTSKVNLVKISS
                     TVSSPRDTALAAVICSALATVLLALLILCVIYCKRQFMEKKPSCKLPSLCLTVK"
BASE COUNT      204 a    245 c    247 g    190 t
```

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ORIGIN


  Query Match             30.8%;  Score 460.8;  DB 11;  Length 886;
  Best Local Similarity   81.9%;  Pred. No. 2.5e-86;
  Matches  531;  Conservative    0;  Mismatches  117;  Indels    0;  Gaps    0;

Qy      22 aataaatacatttgataagaaagatggctttaaaagtgctactagaacaagagaaaacgt 81
           |||||| || |||| | |||   |||||  | || || ||||    |||   ||    |
Db      49 AATAAACACGTTTGGTGAGAGCCATGGCACTCAAGGTCCTACCTCTACACAGGACGGTGC 108

Qy      82 ttttcactcttttagtattactaggctatttgtcatgtaaagtgacttgtgaaacaggag 141
           | ||| ||    |  | || |||  | |  || ||||||||||||| ||| ||||| ||||
Db     109 TCTTCGCTGCCATTCTCTTCCTACTCCACCTGGCATGTAAAGTGAGTTGCGAAACCGGAG 168

Qy     142 actgtagacagcaagaattcagggatcggtctggaaactgtgttccctgcaaccagtgtg 201
           | || || ||||| ||||||| |||||| |||||||||||||| | |||||| ||||| |
Db     169 ATTGCAGGCAGCAGGAATTCAAGGATCGATCTGGAAACTGTGTCCTCTGCAAACAGTGCG 228

Qy     202 ggccaggcatggagttgtctaaggaatgtggcttcggctatggggaggatgcacagtgtg 261
           | || |||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db     229 GACCTGGCATGGAGTTGTCCAAGGAATGTGGCTTCGGCTATGGGGAGGATGCACAGTGTG 288

Qy     262 tgacgtgccggctgcacaggttcaaggaggactggggcttccagaaatgcaagccctgtc 321
           || | ||| ||| |||| |||||||||| |||||||| |||||||| || ||||| |||
Db     289 TGCCCTGCAGGCCGCACCGGTTCAAGGAAGACTGGGGTTTCCAGAAGTGTAAGCCATGTG 348

Qy     322 tggactgcgcagtggtgaaccgctttcagaaggcaaattgttcagccaccagtgatgcca 381
           ||||||  ||  |||||||||||||||||| ||| || || |||  ||||||||||||
Db     349 CGGACTGTGCGCTGGTGAACCGCTTTCAGAGGGCCAACTGCTCACACACCAGTGATGCTG 408

Qy     382 tctgcggggactgcttgccaggattttataggaagacgaaacttgtcggctttcaagaca 441
           |||||||||||||| ||||||||||||  ||||||| ||||| || || ||||||||||
Db     409 TCTGCGGGGACTGCCTGCCAGGATTTTACCGGAAGACCAAACTGGTTGGTTTTCAAGACA 468

Qy     442 tggagtgtgtgccttgtggagaccctcctcctccttacgaaccgcactgtgccagcaagg 501
           |||||||||||| || |||||||| |||||||| |||||||| |||||| |||||||||
Db     469 TGGAGTGTGTGCCCTGCGGAGACCCACCTCCTCCCTACGAACCACACTGTACCAGCAAGG 528

Qy     502 tcaacctcgtgaagatcgcgtccacggcctccagcccacgggacacggcgctggctgccg 561
           | ||||| |||||||||| | ||||| | |||||||||| ||||||||||||||||||||
Db     529 TGAACCTTGTGAAGATCTCCTCCACCGTCTCCAGCCCTCGGGACACGGCGCTGGCTGCCG 588

Qy     562 ttatctgcagcgctctggccaccgtcctgctggccctgctcatcctctgtgtcatctatt 621
           | |||||||| |||||||||| || ||||| |||||||||||||| |||||||||| |
Db     589 TCATCTGCAGTGCTCTGGCCACGGTGCTGCTCGCCCTGCTCATCCTGTGTGTCATCTACT 648

Qy     622 gtaagagacagtttatggagaagaaacccagctggtctctgcggtcac 669
           | ||||| ||||| ||||||||||||||||||||     || |  || |
Db     649 GCAAGAGGCAGTTCATGGAGAAGAAACCCAGCTGTAAGCTCCCATCCC 696


RESULT 10
AF167554
LOCUS       AF167554      591 bp    mRNA            ROD       25-MAY-2000
DEFINITION  Mus musculus TAJ-beta1 mRNA, complete cds.
ACCESSION   AF167554
VERSION     AF167554.1  GI:8071641
KEYWORDS    .
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Eby,M.T., Jasmin,A., Kumar,A., Sharma,K. and Chaudhary,P.M.
  TITLE     TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
            Activates the c-Jun N-terminal Kinase Pathway and Mediates
            Caspase-independent Cell Death
  JOURNAL   J. Biol. Chem. 275 (20), 15336-15342 (2000)
   PUBMED   10809768
REFERENCE   2  (bases 1 to 591)
  AUTHORS   Chaudhary,P.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-JUL-1999) Internal Medicine, UT Southwestern Medical
            Center, 5323 Harry Hines Blvd., Dallas, TX 75235-8593, USA
FEATURES             Location/Qualifiers
     source          1. .591
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone_lib="Soares p3NMF19.5"
     CDS             95. .547
                     /note="soluble receptor"
                     /codon_start=1
                     /product="TAJ-beta1"
                     /protein_id="AAF71827.1"
                     /db_xref="GI:8071642"
                     /translation="MALKVLPLHRTVLFAAILFLLHLACKVSCETGDCRQQEFKDRSG
                     NCVLCKQCGPGMELSKECGFGYGEDAQCVPCRPHRFKEDWGFQKCKPCADCALVNRFQ
                     RANCSHTSDAVCGDCLPGFYRKTKLVGFQDMECVPCGDPPPPYEPHCE"
BASE COUNT      148 a    145 c    175 g    123 t
ORIGIN


  Query Match             21.8%;  Score 326.6;  DB 11;  Length 591;
  Best Local Similarity   78.2%;  Pred. No. 2.7e-58;
  Matches  392;  Conservative    0;  Mismatches  109;  Indels    0;  Gaps    0;

Qy      18 caacaataaatacatttgataagaaagatggctttaaaagtgctactagaacaagagaaa 77
           ||  |||||| || |||| | |||   |||||  | || || ||||    |||   ||
Db      68 CAGGAATAAACACGTTTGGTGAGAGCCATGGCACTCAAGGTCCTACCTCTACACAGGACG 127

Qy      78 acgtttttcactcttttagtattactaggctatttgtcatgtaaagtgacttgtgaaaca 137
             | | ||| ||    |  | || |||  | |  || ||||||||||||| ||| |||||
Db     128 GTGCTCTTCGCTGCCATTCTCTTCCTACTCCACCTGGCATGTAAAGTGAGTTGCGAAACC 187

Qy     138 ggagactgtagacagcaagaattcagggatcggtctggaaactgtgttccctgcaaccag 197
           |||||| || || |||||| ||||||| |||||| |||||||||||||| | |||||| |||
Db     188 GGAGATTGCAGGCAGCAGGAATTCAAGGATCGATCTGGAAACTGTGTCCTCTGCAAACAG 247

Qy     198 tgtgggccaggcatggagttgtctaaggaatgtggcttcggctatggggaggatgcacag 257
           || || || ||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db     248 TGCGGACCTGGCATGGAGTTGTCCAAGGAATGTGGCTTCGGCTATGGGGAGGATGCACAG 307

Qy     258 tgtgtgacgtgccggctgcacaggttcaaggaggactggggcttccagaaatgcaagccc 317
           |||||| | ||| ||| |||| |||||||||| |||||||| |||||||| || |||||
Db     308 TGTGTGCCCTGCAGGCCGCACCGGTTCAAGGAAGACTGGGGTTTCCAGAAGTGTAAGCCA 367

Qy     318 tgtctggactgcgcagtggtgaaccgctttcagaaggcaaattgttcagccaccagtgat 377
           |||  |||||| ||  |||||||||||||||||| ||| || || |||  ||||||||||
Db     368 TGTGCGGACTGTGCGCTGGTGAACCGCTTTCAGAGGGCCAACTGCTCACACACCAGTGAT 427

Qy     378 gccatctgcggggactgcttgccaggattttataggaagacgaaacttgtcggctttcaa 437
           ||  |||||||||||||| |||||||| |||||||  ||||| || || ||||||
Db     428 GCTGTCTGCGGGGACTGCCTGCCAGGATTTTACCGGAAGACCAAACTGGTTGGTTTTCAA 487

Qy     438 gacatggagtgtgtgccttgtggagaccctcctcctccttacgaaccgcactgtgccagc 497
           |||||||||||||||| || |||||||| |||||||| |||||||| |||||||    |
Db     488 GACATGGAGTGTGTGCCCTGCGGAGACCCACCTCCTCCCTACGAACCACACTGTGAGTGA 547

Qy     498 aaggtcaacctcgtgaagatc 518
              | |||      | ||| |
Db     548 TGTGCCAAGTGGCAGCAGACC 568


RESULT 11
AL353136/c
LOCUS       AL353136   188351 bp    DNA             HTG       10-AUG-2000
DEFINITION  Homo sapiens chromosome X clone RP11-133K18, *** SEQUENCING IN
            PROGRESS ***, 16 unordered pieces.
ACCESSION   AL353136
VERSION     AL353136.6  GI:9796991
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

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REFERENCE   1  (bases 1 to 188351)
  AUTHORS   Pavitt,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-AUG-2000) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
            requests: clonerequest@sanger.ac.uk
COMMENT     On Aug 12, 2000 this sequence version replaced gi:9368011.
            -------------- Genome Center
            Center: Sanger Centre
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            -------------- Project Information
            Center project name: bA133K18
            -------------- Summary Statistics
            Assembly program: XGAP4; version 4.5
            Sequencing vector: plasmid; L08752; 100% of reads
            Chemistry: Dye-terminator Big Dye; 100% of reads
            Consensus quality: 176827 bases at least Q40
            Consensus quality: 181768 bases at least Q30
            Consensus quality: 184650 bases at least Q20
            Insert size: 186851; sum-of-contigs
            Insert size: 162009; 18.4% error; agarose-fp
            Quality coverage: 3.49x in Q20 bases; sum-of-contigs Quality
            coverage: 4.02x in Q20 bases; agarose-fp
            --------------
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 16 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *       1    25437: contig of 25437 bp in length
            *   25438 25537: gap of      100 bp
            *   25538    27653: contig of 2116 bp in length
            *   27654 27753: gap of      100 bp
            *   27754    45836: contig of 18083 bp in length
            *   45837 45936: gap of      100 bp
            *   45937    58298: contig of 12362 bp in length
            *   58299 58398: gap of      100 bp
            *   58399    63898: contig of 5500 bp in length
            *   63899 63998: gap of      100 bp
            *   63999    70792: contig of 6794 bp in length
            *   70793 70892: gap of      100 bp
            *   70893    83402: contig of 12510 bp in length
            *   83403 83502: gap of      100 bp
            *   83503   112513: contig of 29011 bp in length
            *  112514 112613: gap of      100 bp
            *  112614   120587: contig of 7974 bp in length
            *  120588 120687: gap of      100 bp
            *  120688   126817: contig of 6130 bp in length
            *  126818 126917: gap of      100 bp
            *  126918   135398: contig of 8481 bp in length
            *  135399 135498: gap of      100 bp
            *  135499   149082: contig of 13584 bp in length
            *  149083 149182: gap of      100 bp
            *  149183   157907: contig of 8725 bp in length
            *  157908 158007: gap of      100 bp
            *  158008   163704: contig of 5697 bp in length
            *  163705 163804: gap of      100 bp
            *  163805   175258: contig of 11454 bp in length
            *  175259 175358: gap of      100 bp
            *  175359   188351: contig of 12993 bp in length.
FEATURES             Location/Qualifiers
     source          1. .188351
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /clone="RP11-133K18"
                     /clone_lib="RPCI-11.1"
     misc_feature    1. .25437
                     /note="assembly_fragment:01650
                     clone_end:SP6
                     vector_side:left"
     misc_feature    25538. .27653
                     /note="assembly_fragment:00293
                     fragment_chain:1"
     misc_feature    27754. .45836
                     /note="assembly_fragment:01209
                     fragment_chain:1"
     misc_feature    45937. .58298
                     /note="assembly_fragment:01684
                     fragment_chain:1"
     misc_feature    58399. .63898
                     /note="assembly_fragment:00037
                     fragment_chain:1"
     misc_feature    63999. .70792
                     /note="assembly_fragment:01432
                     fragment_chain:2"
     misc_feature    70893. .83402
                     /note="assembly_fragment:00471
                     fragment_chain:2"
     misc_feature    83503. .112513
                     /note="assembly_fragment:00822
                     fragment_chain:2"
     misc_feature    112614. .120587
                     /note="assembly_fragment:00509
                     fragment_chain:3"
     misc_feature    120688. .126817
                     /note="assembly_fragment:01092
                     fragment_chain:3"
     misc_feature    126918. .135398
                     /note="assembly_fragment:00273"
     misc_feature    135499. .149082
                     /note="assembly_fragment:00291"
     misc_feature    149183. .157907
                     /note="assembly_fragment:01278"
     misc_feature    158008. .163704
                     /note="assembly_fragment:00964
                     fragment_chain:4"
     misc_feature    163805. .175258
                     /note="assembly_fragment:00415
                     fragment_chain:4"
     misc_feature    175359. .188351
                     /note="assembly_fragment:00856
                     fragment_chain:4
                     clone_end:T7
                     vector_side:right"
BASE COUNT    57974 a  35482 c  35967 g  57418 t   1510 others
ORIGIN


  Query Match             4.9%;  Score 73;  DB 73;  Length 188351;
  Best Local Similarity   60.2%;  Pred. No. 4.1e-05;
  Matches  121;  Conservative    0;  Mismatches   80;  Indels    0;  Gaps    0;

Qy    223 aggaatgtggcttcggctatggggaggatgcacagtgtgtgacgtgccggctgcacaggt 282
          |||| ||||| |  ||  | || |  |||||  | ||     | ||||  |  | |||||
Db 143334 AGGATTGTGGTTATGGAGAGGGTGGAGATGCCTACTGCACAGCCTGCCCTCCTCGCAGGT 143275

Qy    283 tcaaggaggactggggcttccagaaatgcaagccctgtctggactgcgcagtggtgaacc 342
           |||      |||||||  ||| | |||  ||   ||  |   ||| || ||  | || |
Db 143274 ACAAAAGCAGCTGGGGCCACCACAGATGTCAGAGTTGCATCACCTGTGCTGTCATCAATC 143215

Qy    343 gctttcagaaggcaaattgttcagccaccagtgatgccatctgcggggactgcttgccag 402
          |  |||||||||  || ||  |||| |||  | ||||  |||| |||||||| |||||
Db 143214 GTGTTCAGAAGGTCAACTGCACAGCTACCTCTAATGCTGTCTGTGGGGACTGTTTGCCCA 143155

Qy    403 gattttataggaagacgaaac 423
          | |    | |    | || ||
Db 143154 GGTGAGCTTGCTTTATGAGAC 143134


RESULT  12
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```
AC023560/c
LOCUS       AC023560   205736 bp    DNA             HTG       12-MAR-2000
DEFINITION  Homo sapiens chromosome 17 clone RP11-85I20 map 17, WORKING DRAFT
            SEQUENCE, 34 unordered pieces.
ACCESSION   AC023560
VERSION     AC023560.2  GI:7229913
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 205736)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 17, clone RP11-85I20
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 205736)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
            Anderson,S., Baldwin,J., Barna,N., Beda,F., Boguslavkiy,L.,
            Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
            Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
            DeArellano,K., Dewar,K., Dodge,S., Domino,M., Doyle,M.,
            Fenestor,J., Ferreira,P., FitzHugh,W., Forrest,C., Gage,D.,
            Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
            Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
            Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
            Klein,J., Landers,T., Largocque,K., Lehoczky,J., Levine,R.,
            Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M.,
            McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Meldrim,J.,
            Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J., Naylor,J.,
            Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Olivar,T.M.,
            Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C.,
            Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S.,
            Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
            Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A.,
            Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B.,
            Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and
            Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-FEB-2000) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Mar 12, 2000 this sequence version replaced gi:6978256.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L6741
                Center clone name: 85_I_20
            -------------- Summary Statistics
                Sequencing vector: M13; M77815; 100% of reads
                Chemistry: Dye-terminator Big Dye; 100% of reads
                Assembly program: Phrap; version 0.960731
                Consensus quality: 178666 bases at least Q40
                Consensus quality: 190940 bases at least Q30
                Consensus quality: 197088 bases at least Q20
                Insert size: 194000; agarose-fp
                Insert size: 202436; sum-of-contigs
                Quality coverage: 4.2 in Q20 bases; agarose-fp
                Quality coverage: 4.0 in Q20 bases; sum-of-contigs
            --------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 34 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *       1     1267: contig of 1267 bp in length
            *    1268  1367: gap of      100 bp
            *    1368     2402: contig of 1035 bp in length
            *    2403  2502: gap of      100 bp
            *    2503     3524: contig of 1022 bp in length
            *    3525  3624: gap of      100 bp
            *    3625     4913: contig of 1289 bp in length
            *    4914  5013: gap of      100 bp
            *    5014     6289: contig of 1276 bp in length
            *    6290  6389: gap of      100 bp
            *    6390     7655: contig of 1266 bp in length
            *    7656  7755: gap of      100 bp
            *    7756     9267: contig of 1512 bp in length
            *    9268  9367: gap of      100 bp
            *    9368    11138: contig of 1771 bp in length
            *   11139  11238: gap of      100 bp
            *   11239    13822: contig of 2584 bp in length
            *   13823  13922: gap of      100 bp
            *   13923    16968: contig of 3046 bp in length
            *   16969  17068: gap of      100 bp
            *   17069    20185: contig of 3117 bp in length
            *   20186  20285: gap of      100 bp
            *   20286    22634: contig of 2349 bp in length
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            *   27013  27112: gap of      100 bp
            *   27113    29342: contig of 2230 bp in length
            *   29343  29442: gap of      100 bp
            *   29443    33381: contig of 3939 bp in length
            *   33382  33481: gap of      100 bp
            *   33482    36562: contig of 3081 bp in length
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            *   36663    40982: contig of 4320 bp in length
            *   40983  41082: gap of      100 bp
            *   41083    45520: contig of 4438 bp in length
            *   45521  45620: gap of      100 bp
            *   45621    50623: contig of 5003 bp in length
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            *   55711    61038: contig of 5328 bp in length
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            *   73580    80554: contig of 6975 bp in length
            *   80555  80654: gap of      100 bp
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            *   89314  89413: gap of      100 bp
            *   89414    98132: contig of 8719 bp in length
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            *   98233   107469: contig of 9237 bp in length
            *  107470 107569: gap of      100 bp
            *  107570   117873: contig of 10304 bp in length
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            *  117974   130973: contig of 13000 bp in length
            *  130974 131073: gap of      100 bp
            *  131074   143236: contig of 12163 bp in length
            *  143237 143336: gap of      100 bp
            *  143337   154478: contig of 11142 bp in length
            *  154479 154578: gap of      100 bp
            *  154579   169967: contig of 15389 bp in length
            *  169968 170067: gap of      100 bp
            *  170068   187347: contig of 17280 bp in length
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  Matches  121;  Conservative    0;  Mismatches   80;  Indels    0;  Gaps    0;

Qy     223 aggaatgtggcttcggctatggggaggatgcacagtgtgtgacgtgccggctgcacaggt 282
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Db   79395 AGGATTGTGGTTATGGAGAGGGTGGAGATGCCTACTGCACAGCCTGCCCTCCTCGCAGGT 79336

Qy     283 tcaaggaggactggggcttccagaaatgcaagccctgtctggactgcgcagtggtgaacc 342
             |||      |||||||  ||| | |||  ||   ||  |   ||| || ||  | || |
Db   79335 ACAAAAGCAGCTGGGGCCACCACAGATGTCAGAGTTGCATCACCTGTGCTGTCATCAATC 79276

Qy     343 gctttcagaaggcaaattgttcagccaccagtgatgccatctgcggggactgcttgccag 402
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Qy     403 gattttataggaagacgaaac 423
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RESULT  13
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DEFINITION  Homo sapiens chromosome 17 clone RP11-85I20 map 17, WORKING DRAFT
            SEQUENCE, 34 unordered pieces.
ACCESSION   AC023560
VERSION     AC023560.2  GI:7229913
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 205736)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 17, clone RP11-85I20
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 205736)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
            Anderson,S., Baldwin,J., Barna,N., Beda,F., Boguslavkiy,L.,
            Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
            Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
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            Klein,J., Landers,T., Largocque,K., Lehoczky,J., Levine,R.,
            Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M.,
            McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Meldrim,J.,
            Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J., Naylor,J.,
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            Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
            Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A.,
            Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B.,
            Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and
            Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-FEB-2000) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Mar 12, 2000 this sequence version replaced gi:6978256.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L6741
                Center clone name: 85_I_20
            -------------- Summary Statistics
                Sequencing vector: M13; M77815; 100% of reads
                Chemistry: Dye-terminator Big Dye; 100% of reads
                Assembly program: Phrap; version 0.960731
                Consensus quality: 178666 bases at least Q40
                Consensus quality: 190940 bases at least Q30
                Consensus quality: 197088 bases at least Q20
                Insert size: 194000; agarose-fp
                Insert size: 202436; sum-of-contigs
                Quality coverage: 4.2 in Q20 bases; agarose-fp
                Quality coverage: 4.0 in Q20 bases; sum-of-contigs
            --------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 34 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
```

```
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*        1     1267: contig of 1267 bp in length
*     1268 1367: gap of      100 bp
*     1368     2402: contig of 1035 bp in length
*     2403 2502: gap of      100 bp
*     2503     3524: contig of 1022 bp in length
*     3525 3624: gap of      100 bp
*     3625     4913: contig of 1289 bp in length
*     4914 5013: gap of      100 bp
*     5014     6289: contig of 1276 bp in length
*     6290 6389: gap of      100 bp
*     6390     7655: contig of 1266 bp in length
*     7656 7755: gap of      100 bp
*     7756     9267: contig of 1512 bp in length
*     9268 9367: gap of      100 bp
*     9368    11138: contig of 1771 bp in length
*    11139 11238: gap of      100 bp
*    11239    13822: contig of 2584 bp in length
*    13823 13922: gap of      100 bp
*    13923    16968: contig of 3046 bp in length
*    16969 17068: gap of      100 bp
*    17069    20185: contig of 3117 bp in length
*    20186 20285: gap of      100 bp
*    20286    22634: contig of 2349 bp in length
*    22635 22734: gap of      100 bp
*    22735    27012: contig of 4278 bp in length
*    27013 27112: gap of      100 bp
*    27113    29342: contig of 2230 bp in length
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*    33482    36562: contig of 3081 bp in length
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*    36663    40982: contig of 4320 bp in length
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*    41083    45520: contig of 4438 bp in length
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*    45621    50623: contig of 5003 bp in length
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*    50724    55610: contig of 4887 bp in length
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*    55711    61038: contig of 5328 bp in length
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*    80655    89313: contig of 8659 bp in length
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*    98233   107469: contig of 9237 bp in length
*   107470 107569: gap of      100 bp
*   107570   117873: contig of 10304 bp in length
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*   131074   143236: contig of 12163 bp in length
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*   143337   154478: contig of 11142 bp in length
*   154479 154578: gap of      100 bp
*   154579   169967: contig of 15389 bp in length
*   169968 170067: gap of      100 bp
*   170068   187347: contig of 17280 bp in length
*   187348 187447: gap of      100 bp
*   187448   205736: contig of 18289 bp in length.
FEATURES             Location/Qualifiers
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RESULT 14
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DEFINITION  Rattus norvegicus C2-HC type zinc finger protein r-MyT13 mRNA,
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ACCESSION   U67080
VERSION     U67080.1  GI:1531644
KEYWORDS    .
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 3618)
  AUTHORS   Bellefroid,E.J., Bourguignon,C., Hollemann,T., Ma,Q.,
            Anderson,D.J., Kintner,C. and Pieler,T.
  TITLE     X-MyT1, a Xenopus C2HC-type zinc finger protein with a regulatory
            function in neuronal differentiation
  JOURNAL   Cell 87 (7), 1191-1202 (1996)
  MEDLINE   97134666
REFERENCE   2  (bases 1 to 3618)
  AUTHORS   Bellefroid,E.J., Bourguignon,C., Hollemann,T., Ma,Q.,
            Anderson,D.J., Kintner,C. and Pieler,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-AUG-1996) Biochemistry, Gottingen University,
            Humboldtallee 23, Goettingen 37073, Germany
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                     KGSLSLLEQAIALQAERGSVFHHTYKELDRFLLDHLARQRRQPKVTDASGRQIFNNKH
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                     GCTGRGHVNSNRNTHRSLSGCPIAAAEKLAMTQDKSQLDSSQTGQGPEQAHRVNLVKQ
                     IEFNFRSQAITSPRASASKEQEKFGKVPFDYASFDAQVFGKRPLLQTGQGQKAPPFPE
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                     DILSNKPQSLRAKGAEIEVDENGTLDLSMKKNRILDKSIGGTSSHTTIATPSSSPFKA
                     SSLLVNAAFYQALCDQEGWNVPINYSKSHGKTEEEKEKDPVNSLENLEEKKFAGEASI
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ORIGIN


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Qy    1445 caagtatttttttaaaaactaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 1496
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Db    3565 GACATTTTATATTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3616


RESULT 15
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LOCUS       ASPDXA3H     6105 bp    DNA             SYN       24-JAN-1996
DEFINITION  Artificial sequences cloning vector DNA pDXA-3H.
ACCESSION   X85119
VERSION     X85119.1  GI:717174
KEYWORDS    cloning vector; expression vector.
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 6105)
  AUTHORS   Manstein,D.J., Schuster,H.P., Morandini,P. and Hunt,D.M.
  TITLE     Cloning vectors for the production of proteins in Dictyostelium
            discoideum
  JOURNAL   Gene 162 (1), 129-134 (1995)
  MEDLINE   96009890
REFERENCE   2  (bases 1 to 6105)
  AUTHORS   Manstein,D.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-MAR-1995) D.J. Manstein, National Institute for
            Medical Research, The Ridgeway, Mill Hill, London NW7 1AA, UK
COMMENT     Related sequences: Gene 19, 327-336(1982) and M55298.
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BASE COUNT     1856 a   1263 c   1184 g   1801 t      1 others
ORIGIN


  Query Match             4.3%;  Score 63.8;  DB 12;  Length 6105;
  Best Local Similarity   62.0%;  Pred. No. 0.0027;
  Matches  101;  Conservative    0;  Mismatches   62;  Indels    0;  Gaps    0;

Qy    1334 agtagatcagaactctgttcccagcataagatttgggggaacctgatgagtttttttttt 1393
           ||| |||| || ||| || ||   |||    |  |  | | |||||   | |||||| |
Db    6054 AGTGGATCCGAGCTCGGTACCATCCATTTTTTAAGCTTGGATCTGATTTTTATTTTTTAT 5995

Qy    1394 gcatctttaataatttcttgtatgttgtagagtatgttttaaaataaatttcaagtattt 1453
             |  || | | |||| || || |   ||    |      |||| ||| |     |||
Db    5994 TTAATTTAATTTATTTGTTTTAAGAAATAAGAAAAAAAAAAAAAAAAAATCTTTTTATGC 5935

Qy    1454 tttttaaaaactaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 1496
             | | ||||  |||||||||||||||||||||||||||||||
Db    5934 AATCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5892


Search completed: March  3, 2001, 04:45:22
Job time: 18969 sec
```

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 2, 2001, 23:32:11 ; Search time 88.06 Seconds
(without alignments)
6381.914 Million cell updates/sec

Title: US-09-380-276A-7
Perfect score: 1496
Sequence: 1 gggaacgtagaactctccaa.....aaaaaaaaaaaaaaaaaaaa 1496

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_36:*
1: /cgn2_2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /cgn2_2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
3: /cgn2_2/gcgdata/geneseq/geneseqn/NA1982.DAT:*
4: /cgn2_2/gcgdata/geneseq/geneseqn/NA1983.DAT:*
5: /cgn2_2/gcgdata/geneseq/geneseqn/NA1984.DAT:*
6: /cgn2_2/gcgdata/geneseq/geneseqn/NA1985.DAT:*
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21: /cgn2_2/gcgdata/geneseq/geneseqn/NA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1496	100.0	1496	19	V33362	Nucleotide sequenc
	2	1494.4	99.9	1502	20	X08689	Novel nucleotide s
	3	1421.4	95.0	1489	20	X23415	Human hAPO4-alpha
	4	1288.8	86.1	1704	19	V33361	Nucleotide sequenc
	5	1276.4	85.3	2185	20	X24978	Human TRAIN-R cDNA
	6	835.6	55.9	987	20	X59346	Human NTR-5 cDNA.
	7	741	49.5	1678	20	X23413	Mouse mAPO4-alpha
	8	460.8	30.8	886	20	X23414	Mouse mAPO4-alpha
	9	460.8	30.8	942	20	X24977	Mouse TRAIN-R (lon
	10	460.8	30.8	981	20	X87394	Mouse STRIFE1 (Tan
	11	447.2	29.9	893	20	X84622	Human TNFR superfa
	12	362.6	24.2	538	20	X59345	Mouse NTR-5 cDNA.
	13	361.6	24.2	371	19	V11422	Human secreted pro
	14	326.6	21.8	591	20	X23417	Mouse mAPO4-gamma
	15	326.6	21.8	599	20	X24976	Mouse TRAIN-R (sho
	16	326.6	21.8	623	20	X84623	Mouse TNFR superfa
	17	326.6	21.8	636	21	Z92408	cDNA encoding muri
	18	326.6	21.8	655	20	X87395	Mouse STRIFE2 (Tan
	19	154.8	10.3	932	21	Z92411	cDNA encoding huma
	20	121.8	8.1	1133	20	X23416	Rat rAPO4-alpha DN
	21	90.4	6.0	791	20	X24979	Clone GJ156 encodi
	22	87.4	5.8	181	19	V11423	Human secreted pro
	23	87.4	5.8	201	20	V86655	EST clone AX92. H
	24	82	5.5	396	20	X23418	Mouse mAPO4-beta D
	25	81.2	5.4	546	21	Z92410	cDNA encoding huma
	26	77.8	5.2	474	21	Z92409	cDNA encoding huma
	27	57.8	3.9	1584	21	D00015	Scorpion protein d
	28	57	3.8	1443	21	A26291	Human secreted pro
	29	56.8	3.8	1883	19	V59670	Human secreted pro
	30	54.8	3.7	1558	17	T28255	Survival motor neu
	31	54.8	3.7	1560	17	T18828	Human survival mot
	32	54.8	3.7	1582	17	T28259	Survival motor neu
	33	54.8	3.7	1582	17	T18831	Human survival mot
	34	54.4	3.6	2271	20	V84632	Human secreted pro
	35	54.4	3.6	2276	20	V84583	Human secreted pro
c	36	54.4	3.6	3138	12	Q11712	Shuttle vector pMU
	37	54.2	3.6	1969	20	X60804	Human secreted pro
	38	53.6	3.6	3809	21	A23440	cDNA encoding huma
	39	53	3.5	2007	19	V40754	C. felis esterase,
c	40	53	3.5	2007	19	V40755	C. felis esterase,
	41	52.8	3.5	664	21	A26336	Human secreted pro
	42	52.8	3.5	2933	21	Z93703	PRO172 DNA35916-11
	43	52.8	3.5	5173	18	T89783	Human Immunodefici
	44	52.6	3.5	1420	18	T72167	Alzheimer's diseas
	45	52.6	3.5	3238	16	Q83532	Sequence encoding

ALIGNMENTS

RESULT 1
V33362
ID V33362 standard; cDNA to mRNA; 1496 BP.
XX
AC V33362;
XX
DT 02-DEC-1998 (first entry)
XX
DE Nucleotide sequence of human beta-OAF065.
XX
KW Human; beta-OAF065; stroma cell; antibody; inflammatory;
KW cytokine-mediated disease; rheumatism; ulcerative colitis; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 45..1316
FT /*tag= a
FT /product= "human beta-OAF065 protein"
FT sig_peptide 45..119
FT /*tag= b
FT mat_peptide 120..1313
FT /*tag= c
FT /transl_except= (pos:711..713, aa= Pro)
FT /transl_except= (pos:714..716, aa= Arg)
XX
PN WO9838304-A1.
XX
PD 03-SEP-1998.
XX
PF 26-FEB-1998; 98WO-JP00799.
XX
PR 27-FEB-1997; 97JP-0043143.
XX
PA (ONOY) ONO PHARM CO LTD.

```
XX
PI   Fukushima D,  Konishi M,  Tada H;
XX
DR   WPI; 1998-481205/41.
DR   P-PSDB; W70387.
XX
PT   Membrane polypeptide expressed by human stroma cells, and antibodies
PT   recognising it - for treatment of inflammatory and other
PT   cytokine-mediated diseases.
XX
PS   Disclosure; Pages 40-41; 54pp; Japanese.
XX
CC   This is the nucleotide sequence of the human beta-OAF065, used in
CC   the method of the invention.  The process involves the use of peptides
CC   expressed by stroma cells, and its antibodies are used for in the
CC   prevention and treatment of inflammatory and other cytokine-mediated
CC   diseases such as rheumatism, ulcerative colitis.
XX
SQ   Sequence 1496 BP; 388 A; 360 C; 372 G; 376 T; 0 other;


  Query Match            100.0%;  Score 1496;  DB 19;  Length 1496;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1496;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 gggaacgtagaactctccaacaataaatacatttgataagaaagatggctttaaaagtgc 60
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Db      1 gggaacgtagaactctccaacaataaatacatttgataagaaagatggctttaaaagtgc 60

Qy     61 tactagaacaagagaaaacgtttttcactcttttagtattactaggctatttgtcatgta 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 tactagaacaagagaaaacgtttttcactcttttagtattactaggctatttgtcatgta 120

Qy    121 aagtgacttgtgaaacaggagactgtagacagcaagaattcagggatcggtctggaaact 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 aagtgacttgtgaaacaggagactgtagacagcaagaattcagggatcggtctggaaact 180

Qy    181 gtgttccctgcaaccagtgtgggccaggcatggagttgtctaaggaatgtggcttcggct 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 gtgttccctgcaaccagtgtgggccaggcatggagttgtctaaggaatgtggcttcggct 240

Qy    241 atggggaggatgcacagtgtgtgacgtgccggctgcacaggttcaaggaggactggggct 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 atggggaggatgcacagtgtgtgacgtgccggctgcacaggttcaaggaggactggggct 300

Qy    301 tccagaaatgcaagccctgtctggactgcgcagtggtgaaccgctttcagaaggcaaatt 360
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Db    301 tccagaaatgcaagccctgtctggactgcgcagtggtgaaccgctttcagaaggcaaatt 360

Qy    361 gttcagccaccagtgatgccatctgcggggactgcttgccaggattttataggaagacga 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 gttcagccaccagtgatgccatctgcggggactgcttgccaggattttataggaagacga 420

Qy    421 aacttgtcggctttcaagacatggagtgtgtgccttgtggagaccctcctcctccttacg 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 aacttgtcggctttcaagacatggagtgtgtgccttgtggagaccctcctcctccttacg 480

Qy    481 aaccgcactgtgccagcaaggtcaacctcgtgaagatcgcgtccacggcctccagcccac 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 aaccgcactgtgccagcaaggtcaacctcgtgaagatcgcgtccacggcctccagcccac 540

Qy    541 gggacacggcgctggctgccgttatctgcagcgctctggccaccgtcctgctggccctgc 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 gggacacggcgctggctgccgttatctgcagcgctctggccaccgtcctgctggccctgc 600

Qy    601 tcatcctctgtgtcatctattgtaagagacagtttatggagaagaaacccagctggtctc 660
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Qy    661 tgcggtcacaggacattcagtacaacggctctgagctgtcgtgtcttgacagacctcagc 720
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Qy    721 tccacgaatatgcccacagagcctgctgccagtgccgccgtgactcagtgcagacctgcg 780
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Qy    781 ggccggtgcgcttgctcccatccatgtgctgtgaggaggcctgcagccccaacccggcga 840
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Db    781 ggccggtgcgcttgctcccatccatgtgctgtgaggaggcctgcagccccaacccggcga 840

Qy    841 ctcttggttgtggggtgcattctgcagccagtcttcaggcaagaaacgcaggcccagccg 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    901 gggagatggtgccgactttcttcggatccctcacgcagtccatctgtggcgagttttcag 960
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Qy    961 atgcctggcctctgatgcagaatcccatgggtggtgacaacatctctttttgtgactctt 1020
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Db    961 atgcctggcctctgatgcagaatcccatgggtggtgacaacatctctttttgtgactctt 1020

Qy   1021 atcctgaactcactggagaagacattcattctctcaatccagaacttgaaagctcaacgt 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 atcctgaactcactggagaagacattcattctctcaatccagaacttgaaagctcaacgt 1080

Qy   1081 ctttggattcaaatagcagtcaagatttggttggtggggctgttccagtccagtctcatt 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ctttggattcaaatagcagtcaagatttggttggtggggctgttccagtccagtctcatt 1140

Qy   1141 ctgaaaactttacagcagctactgatttatctagatataacaacacactggtagaatcag 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ctgaaaactttacagcagctactgatttatctagatataacaacacactggtagaatcag 1200

Qy   1201 catcaactcaggatgcactaactatgagaagccagctagatcaggagagtggcgctatca 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1261 tccacccagccactcagacgtccctccaggtaaggcagcgactgggttccctgtgaacac 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1321 agcactgacttacagtagatcagaactctgttcccagcataagatttgggggaacctgat 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 agcactgacttacagtagatcagaactctgttcccagcataagatttgggggaacctgat 1380

Qy   1381 gagtttttttttttgcatctttaataatttcttgtatgttgtagagtatgttttaaaataa 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 gagtttttttttttgcatctttaataatttcttgtatgttgtagagtatgttttaaaataa 1440

Qy   1441 atttcaagtatttttttttaaaaactaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 1496
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 atttcaagtatttttttttaaaaactaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 1496


RESULT   2
X08689
ID   X08689 standard; cDNA; 1502 BP.
XX
AC   X08689;
XX
DT   27-SEP-1999  (first entry)
XX
DE   Novel nucleotide sequence encoding new protein (Clone AX92_3).
XX
KW   Polynucleotide; protein; nutrition; cytokine; cell proliferation;
KW   cell differentiation; immunostimulation; immunosuppression;
KW   haematopoiesis regulation; tissue growth; activin; inhibin;
KW   chemotaxis; chemokinesis; haemostasis; thrombolysis; receptor;
KW   ligand; anti-inflammatory; tumour suppression; gene therapy; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             51..1322
```

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FT                   /*tag= a
FT                   /product= "Novel protein"
XX
PN   WO9920644-A1.
XX
PD   29-APR-1999.
XX
PF   16-OCT-1998;   98WO-US22034.
XX
PR   18-OCT-1997;   97US-0955557.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Agostino MJ,  Bowman MR,  Evans C,  Jacobs K,  Lavallie ER;
PI   McCoy JM,  Merberg D,  Racie LA,  Spaulding V,  Treacy M;
XX
DR   WPI; 1999-288272/24.
DR   P-PSDB; W85724.
XX
PT   New polynucleotides encoding secreted human proteins
XX
PS   Claim 32; Page 116; 136pp; English.
XX
CC   The new human secreted proteins are encoded by polynucleotides
CC   obtained from human placenta, adult testes, fetal kidney, fetal
CC   brain, adult brain, adult brain and adult blood cDNA libraries.
CC   The polynucleotides and proteins are predicted to have biological
CC   activities which would make them suitable for treating, preventing or
CC   ameliorating medical conditions in humans and animals. Suggested
CC   activities include nutritional activity, cytokine and cell
CC   proliferation/differentiation activity, immune stimulating (e.g. as
CC   vaccines) or suppressing activity, haematopoiesis regulating
CC   activity, tissue growth activity, activin/inhibin activity,
CC   chemotactic/chemokinetic activity, haemostatic and thrombolytic
CC   activity, receptor/ligand activity, anti-inflammatory activity,
CC   cadherin/tumour invasion suppressor activity, and tumour inhibition
CC   activity.  The polynucleotides are also stated to be useful for gene
CC   therapy. The sequences are identified by a secretory leader
CC   sequence motif in the polynucleotide and it is thought that the
CC   encoded proteins have biological activity by virtue of their secreted
CC   nature. This clone was designated AX92_3. A probe for this clone is
CC   described in X08704.
XX
SQ   Sequence 1502 BP; 388 A; 362 C; 375 G; 377 T; 0 other;
```

Query Match 99.9%; Score 1494.4; DB 20; Length 1502;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1495; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 gggaacgtagaactctccaacaataaatacatttgataagaaagatggctttaaaagtgc 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7 gggaacgtagaactctccaacaataaatacatttgataagaaagatggctttaaaagtgc 66

Qy     61 tactagaacaagagaaaacgtttttcactcttttagtattactaggctatttgtcatgta 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     67 tactagaacaagagaaaacgtttttcactcttttagtattactaggctatttgtcatgta 126

Qy    121 aagtgacttgtgaaacaggagactgtagacagcaagaattcagggatcggtctggaaact 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    127 aagtgacttgtgaaacaggagactgtagacagcaagaattcagggatcggtctggaaact 186

Qy    181 gtgttccctgcaaccagtgtgggccaggcatggagttgtctaaggaatgtggcttcggct 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    187 gtgttccctgcaaccagtgtgggccaggcatggagttgtctaaggaatgtggcttcggct 246

Qy    241 atggggaggatgcacagtgtgtgacgtgccggctgcacaggttcaaggaggactggggct 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    247 atggggaggatgcacagtgtgtgacgtgccggctgcacaggttcaaggaggactggggct 306

Qy    301 tccagaaatgcaagccctgtctggactgcgcagtggtgaaccgctttcagaaggcaaatt 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    307 tccagaaatgcaagccctgtctggactgcgcagtggtgaaccgctttcagaaggcaaatt 366

Qy    361 gttcagccaccagtgatgccatctgcggggactgcttgccaggattttataggaagacga 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    367 gttcagccaccagtgatgccatctgcggggactgcttgccaggattttataggaagacga 426

Qy    421 aacttgtcggctttcaagacatggagtgtgtgccttgtggagaccctcctcctccttacg 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    427 aacttgtcggctttcaagacatggagtgtgtgccttgtggagaccctcctcctccttacg 486

Qy    481 aaccgcactgtgccagcaaggtcaacctcgtgaagatcgcgtccacggcctccagcccac 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    487 aaccgcactgtgccagcaaggtcaacctcgtgaagatcgcgtccacggcctccagcccac 546

Qy    541 gggacacggcgctggctgccgttatctgcagcgctctggccaccgtcctgctggccctgc 600
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Db    547 gggacacggcgctggctgccgttatctgcagcgctctggccaccgtcctgctggccctgc 606

Qy    601 tcatcctctgtgtcatctattgtaagagacagtttatggagaagaaacccagctggtctc 660
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Qy    661 tgcggtcacaggacattcagtacaacggctctgagctgtcgtgtcttgacagacctcagc 720
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Qy    721 tccacgaatatgcccacagagcctgctgccagtgccgccgtgactcagtgcagacctgcg 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    727 tccacgaatatgcccacagagcctgctgccagtgccgccgtgactcagtgcagacctgcg 786

Qy    781 ggccggtgcgcttgctcccatccatgtgctgtgaggaggcctgcagccccaacccggcga 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    787 ggccggtgcgcttgctcccatccatgtgctgtgaggaggcctgcagccccaacccggcga 846

Qy    841 ctcttggttgtggggtgcattctgcagccagtcttcaggcaagaaacgcaggcccagccg 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    847 ctcttggttgtggggtgcattctgcagccagtcttcaggcaagaaacgcaggcccagccg 906

Qy    901 gggagatggtgccgactttcttcggatccctcacgcagtccatctgtggcgagttttcag 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    907 gggagatggtgccgactttcttcggatccctcacgcagtccatctgtggcgagttttcag 966

Qy    961 atgcctggcctctgatgcagaatcccatgggtggtgacaacatctctttttgtgactctt 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    967 atgcctggcctctgatgcagaatcccatgggtggtgacaacatctctttttgtgactctt 1026

Qy   1021 atcctgaactcactggagaagacattcattctctcaatccagaacttgaaagctcaacgt 1080
          ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1027 atcctgaactcgctggagaagacattcattctctcaatccagaacttgaaagctcaacgt 1086

Qy   1081 ctttggattcaaatagcagtcaagatttggttggtggggctgttccagtccagtctcatt 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1087 ctttggattcaaatagcagtcaagatttggttggtggggctgttccagtccagtctcatt 1146

Qy   1141 ctgaaaacttacagcagctactgatttatctagatataacaacacactggtagaatcag 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1147 ctgaaaacttacagcagctactgatttatctagatataacaacacactggtagaatcag 1206

Qy   1201 catcaactcaggatgcactaactatgagaagccagctagatcaggagagtggcgctatca 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1207 catcaactcaggatgcactaactatgagaagccagctagatcaggagagtggcgctatca 1266

Qy   1261 tccacccagccactcagacgtccctccaggtaaggcagcgactgggttccctgtgaacac 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1267 tccacccagccactcagacgtccctccaggtaaggcagcgactgggttccctgtgaacac 1326

Qy   1321 agcactgacttacagtagatcagaactctgttcccagcataagatttgggggaacctgat 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1327 agcactgacttacagtagatcagaactctgttcccagcataagatttgggggaacctgat 1386

Qy   1381 gagtttttttttttgcatctttaataatttcttgtatgttgtagagtatgttttaaaataa 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1387 gagtttttttttttgcatctttaataatttcttgtatgttgtagagtatgttttaaaataa 1446
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```
Qy   1441 atttcaagtatttttttttaaaaactaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 1496
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1447 atttcaagtatttttttttaaaaactaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 1502
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RESULT 3
X23415
ID X23415 standard; DNA; 1489 BP.
XX
AC X23415;
XX
DT 18-JUN-1999 (first entry)
XX
DE Human hAPO4-alpha DNA.
XX
KW Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
KW developmental abnormality; gestational abnormalitity; prostate cancer;
KW APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
KW cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
KW apoptosis; human; APO4-alpha; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 65..1336
FT /*tag= a
FT /product= "hAPO4-alpha"
XX
PN WO9911791-A2.
XX
PD 11-MAR-1999.
XX
PF 04-SEP-1998; 98WO-US18393.
XX
PR 05-SEP-1997; 97US-0924634.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Chaudhary PM;
XX
DR WPI; 1999-205191/17.
DR P-PSDB; W93581.
XX
PT New Tumor Necrosis Factor family receptor polypeptides and ligands -
PT useful for diagnosis and treatment of prostate cancer and
PT developmental or gestational abnormalities
XX
PS Example IV; Fig 7C; 156pp; English.
XX
CC This invention describes isolated Tumor Necrosis Factor (TNF) family
CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
CC their active fragments. APO4 is useful for diagnosing prostate cancer
CC by determining levels of APO4 in an individual. Prostate cancer can also
CC be treated using APO4 selective binding agents linked to a therapeutic
CC moiety. APO4 polypeptides are also useful for identifying selective
CC binding agents, useful in diagnosis/treatment of disease by binding of
CC agents to the polypeptide/active fragment which is extracellular, or
CC expressed on the cell surface. The binding is preferably performed in
CC vivo. APO4 polypeptides/ active fragments are also useful for screening
CC for agonists and antagonists by binding and observing the changer in APO4
CC activity. Effective pharmacological agents useful in diagnosis or
CC treatment of disease are also identified using APO4 polypeptides/active
CC fragments and APO4 signal transducer molecules that specifically interact
CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4
CC activity. The method is performed in vivo or in vitro. APO polypeptides
CC are all useful as immunogens for preparing antibodies. APO4 is also
CC useful for diagnosis/treatment of developmental or gestational
CC abnormalities. APO8 was transfected to human breast carcinoma cell line
CC MCF-7, and induced apoptosis.
XX
SQ Sequence 1489 BP; 361 A; 366 C; 380 G; 382 T; 0 other;

Query Match 95.0%; Score 1421.4; DB 20; Length 1489;
Best Local Similarity 98.8%; Pred. No. 2.6e-290;
Matches 1443; Conservative 0; Mismatches 16; Indels 2; Gaps 1;

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Qy      7 gtagaactctccaacaataaatacatttgataagaaagatggctttaaaagtgctactag 66
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Db     27 gaagaactctccaacaataaatacatttgataagaaagatggctttaaaagtgctactag 86

Qy     67 aacaagagaaaacgtttttcactcttttagtattactaggctatttgtcatgtaaagtga 126
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     87 aacaagagaaaacgtttttcactcttttagtattactaggctatttgtcatgtaaagtga 146

Qy    127 cttgtgaaacaggagactgtagacagcaagaattcagggatcggtctggaaactgtgttc 186
          |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    147 cttgtgaatcaggagactgtagacagcaagaattcagggatcggtctggaaactgtgttc 206

Qy    187 cctgcaaccagtgtgggccaggcatggagttgtctaaggaatgtggcttcggctatgggg 246
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    207 cctgcaaccagtgtgggccaggcatggagttgtctaaggaatgtggcttcggctatgggg 266

Qy    247 aggatgcacagtgtgtgacgtgccggctgcacaggttcaaggaggactggggcttccaga 306
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db    267 aggatgcacagtgtgtggcgtgccggctgcacaggttcaaggaggactggggcttccaga 326

Qy    307 aatgcaagccctgtctggactgcgcagtggtgaaccgctttcagaaggcaaattgttcag 366
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    327 aatgcaagccctgtctggactgcgcagtggtgaaccgctttcagaaggcaaattgttcag 386

Qy    367 ccaccagtgatgccatctgcggggactgcttgccaggattttataggaagacgaaacttg 426
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    387 ccaccagtgatgccatctgcggggactgcttgccaggattttataggaagacgaaacttg 446

Qy    427 tcggctttcaagacatggagtgtgtgccttgtggagaccctcctcctccttacgaaccgc 486
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    447 tcggctttcaagacatggagtgtgtgccttgtggagaccctcctcctccttacgaaccgc 506

Qy    487 actgtgccagcaaggtcaacctcgtgaagatcgcgtccacggcctccagcccacgggaca 546
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    507 actgtgccagcaaggtcaacctcgtgaagatcgcgtccacggcctccagcccacgggaca 566

Qy    547 cggcgctggctgccgttatctgcagcgctctggccaccgtcctgctggccctgctcatcc 606
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Qy    607 tctgtgtcatctattgtaagagacagtttatggagaagaaacccagctggtctctgcggt 666
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Qy    667 cacaggacattcagtacaacggctctgagctgtcgtgtcttgacagacctcagctccacg 726
          |||||||||||||||||||   |||||||||||||| ||||||||||||||||||||||
Db    687 cacaggacattcagtacaacgagactgagctgtcgtgttttgacagacctcagctccacg 746

Qy    727 aatatgcccacagagcctgctgccagtgccgccgtgactcagtgcagacctgcgggccgg 786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    747 aatatgcccacagagcctgctgccagtgccgccgtgactcagtgcagacctgcgggccgg 806

Qy    787 tgcgcttgctcccatccatgtgctgtgaggaggcctgcagccccaacccggcgactcttg 846
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    807 tgcgcttgctcccatccatgtgctgtgaggaggcctgcagccccaacccggcgactcttg 866

Qy    847 gttgtggggtgcattctgcagccagtcttcaggcaagaaacgcaggcccagccggggaga 906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    907 tggtgccgactttcttcggatccctcacgcagtccatctgtggcgagttttcagatgcct 966
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Db    927 tggtgccgactttcttcggatccctcacgcagtccatctgtggcgagttttcagatgcct 986

Qy    967 ggcctctgatgcagaatcccatgggtggtgacaacatctctttttgtgactcttatcctg 1026
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    987 ggcctctgatgcagaatcccatgggtggtgacaacatctctttttgtgactcttatcctg 1046
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Qy   1027 aactcactggagaagacattcattctctcaatccagaacttgaaagctcaacgtctttgg 1086
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Db   1047 aactcactggagaagacattcattctctcaatccagaacttgaaagctcaacgtctttgg 1106

Qy   1087 attcaaatagcagtcaagatttggttggtggggctgttccagtccagtctcattctgaaa 1146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1107 attcaaatagcagtcaagatttggttggtggggctgttccagtccagtctcattctgaaa 1166

Qy   1147 actttacagcagctactgatttatctagatataacaacacactggtagaatcagcatcaa 1206
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Db   1167 actttacagcagctactgatttatctagatataacaacacactggtagaatcagcatcaa 1226

Qy   1207 ctcaggatgcactaactatgagaagccagctagatcaggagagtggcgctatcatccacc 1266
          |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
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Qy   1267 cagccactcagacgtccctccaggtaaggcagcgactgggttccctgtgaacacagcact 1326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1327 gacttacagtagatcagaactctgttcccagcataagatttggggaacctg--atgagt 1384
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Db   1347 gacttacagtagatcagaactctgttcccagcataagatttggggaacctggatgagtt 1406

Qy   1385 ttttttttgcatctttaataatttcttgtatgttgtagagtatgttttaaaataaattt 1444
          |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   1407 ttttttttgcatctttaataatttcttatatgttgtagagtatgttttaaaataaattt 1466

Qy   1445 caagtatttttttaaaaact 1465
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Db   1467 caagtatttttttaaaaact 1487
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RESULT   4
V33361
ID   V33361 standard; cDNA to mRNA; 1704 BP.
XX
AC   V33361;
XX
DT   02-DEC-1998  (first entry)
XX
DE   Nucleotide sequence of human alpha-OAF065.
XX
KW   Human; alpha-OAF065; stroma cell; antibody; inflammatory;
KW   cytokine-mediated disease; rheumatism; ulcerative colitis; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             45..1298
FT                   /*tag=  a
FT                   /product= "human alpha-OAF065 protein"
FT   sig_peptide     45..119
FT                   /*tag=  b
FT   mat_peptide     120..1295
FT                   /*tag=  c
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FT                   /transl_except= (pos:714..716, aa= Arg)
XX
PN   WO9838304-A1.
XX
PD   03-SEP-1998.
XX
PF   26-FEB-1998;   98WO-JP00799.
XX
PR   27-FEB-1997;   97JP-0043143.
XX
PA   (ONOY ) ONO PHARM CO LTD.
XX
PI   Fukushima D,  Konishi M,  Tada H;
XX
DR   WPI; 1998-481205/41.
DR   P-PSDB; W70386.
XX
PT   Membrane polypeptide expressed by human stroma cells, and antibodies
PT   recognising it - for treatment of inflammatory and other
PT   cytokine-mediated diseases.
XX
PS   Claim 5; Pages 31-32; 54pp; Japanese.
XX
CC   This is the nucleotide sequence of the human alpha-OAF065, used in
CC   the method of the invention.  The process involves the use of peptides
CC   expressed by stroma cells, and its antibodies are used for in the
CC   prevention and treatment of inflammatory and other cytokine-mediated
CC   diseases such as rheumatism, ulcerative colitis.
XX
SQ   Sequence 1704 BP; 429 A; 426 C; 430 G; 419 T; 0 other;
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  Query Match             86.1%;  Score 1288.8;  DB 19;  Length 1704;
  Best Local Similarity   99.8%;  Pred. No. 2.1e-262;
  Matches 1290;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 gggaacgtagaactctccaacaataaatacatttgataagaaagatggctttaaaagtgc 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 gggaacgtagaactctccaacaataaatacatttgataagaaagatggctttaaaagtgc 60

Qy     61 tactagaacaagagaaaacgtttttcactcttttagtattactaggctatttgtcatgta 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 tactagaacaagagaaaacgtttttcactcttttagtattactaggctatttgtcatgta 120

Qy    121 aagtgacttgtgaaacaggagactgtagacagcaagaattcagggatcggtctggaaact 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 aagtgacttgtgaaacaggagactgtagacagcaagaattcagggatcggtctggaaact 180

Qy    181 gtgttccctgcaaccagtgtgggccaggcatggagttgtctaaggaatgtggcttcggct 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 gtgttccctgcaaccagtgtgggccaggcatggagttgtctaaggaatgtggcttcggct 240

Qy    241 atggggaggatgcacagtgtgtgacgtgccggctgcacaggttcaaggaggactggggct 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    301 tccagaaatgcaagccctgtctggactgcgcagtggtgaaccgctttcagaaggcaaatt 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 tccagaaatgcaagccctgtctggactgcgcagtggtgaaccgctttcagaaggcaaatt 360

Qy    361 gttcagccaccagtgatgccatctgcggggactgcttgccaggattttataggaagacga 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 gttcagccaccagtgatgccatctgcggggactgcttgccaggattttataggaagacga 420

Qy    421 aacttgtcggctttcaagacatggagtgtgtgccttgtggagaccctcctcctccttacg 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 aacttgtcggctttcaagacatggagtgtgtgccttgtggagaccctcctcctccttacg 480

Qy    481 aaccgcactgtgccagcaaggtcaacctcgtgaagatcgcgtccacggcctccagcccac 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 aaccgcactgtgccagcaaggtcaacctcgtgaagatcgcgtccacggcctccagcccac 540

Qy    541 gggacacggcgctggctgccgttatctgcagcgctctggccaccgtcctgctggccctgc 600
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Qy    601 tcatcctctgtgtcatctattgtaagagacagtttatggagaagaaacccagctggtctc 660
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Qy    661 tgcggtcacaggacattcagtacaacggctctgagctgtcgtgtcttgacagacctcagc 720
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Db    661 tgcggtcacaggacattcagtacaacggctctgagctgtcgtgtcttgacagacctcagc 720

Qy    721 tccacgaatatgcccacagagcctgctgccagtgccgccgtgactcagtgcagacctgcg 780
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Qy    781 ggccggtgcgcttgctcccatccatgtgctgtgaggaggcctgcagccccaacccggcga 840
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Qy    841 ctcttggttgtggggtgcattctgcagccagtcttcaggcaagaaacgcaggcccagccg 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    901 gggagatggtgccgactttcttcggatccctcacgcagtccatctgtggcgagttttcag 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    961 atgcctggcctctgatgcagaatcccatgggtggtgacaacatctctttttgtgactctt 1020
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Db    961 atgcctggcctctgatgcagaatcccatgggtggtgacaacatctctttttgtgactctt 1020

Qy   1021 atcctgaactcactggagaagacattcattctctcaatccagaacttgaaagctcaacgt 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 atcctgaactcactggagaagacattcattctctcaatccagaacttgaaagctcaacgt 1080

Qy   1081 ctttggattcaaatagcagtcaagatttggttggtggggctgttccagtccagtctcatt 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ctttggattcaaatagcagtcaagatttggttggtggggctgttccagtccagtctcatt 1140

Qy   1141 ctgaaaactttacagcagctactgatttatctagatataacaacacactggtagaatcag 1200
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Qy   1201 catcaactcaggatgcactaactatgagaagccagctagatcaggagagtggcgctatca 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1261 tccacccagccactcagacgtccctccaggta 1292
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Db   1261 tccacccagccactcagacgtccctccaggaa 1292


RESULT   5
X24978
ID   X24978 standard; cDNA; 2185 BP.
XX
AC   X24978;
XX
DT   05-JUL-1999  (first entry)
XX
DE   Human TRAIN-R cDNA.
XX
KW   TRAIN-R; receptor; human; tumour necrosis factor receptor;
KW   agonist; antagonist; cancer; immunological disease; therapy;
KW   cytostatic; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT   sig_peptide     179..253
FT                   /*tag=  b
FT   mat_peptide     254..1429
FT                   /*tag=  c
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XX
PD   18-MAR-1999.
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PF   11-SEP-1998;   98WO-US19030.
XX
PR   06-MAY-1998;   98US-0084422.
PR   12-SEP-1997;   97US-0058631.
XX
PA   (BIOJ ) BIOGEN INC.
XX
PI   Hession C,  Tschopp J;
XX
DR   WPI; 1999-229238/19.
DR   P-PSDB; W98146.
XX
PT   New cysteine-rich tumor necrosis factor receptor
XX
PS   Claim 1; Page 27; 30pp; English.
XX
CC   The present sequence encodes a novel human cysteine-rich tumour
CC   necrosis factor receptor family member termed TRAIN-R (see W98146).
CC   It is a composite of 2 overlapping lambda gt10 clones (GJ159 and
CC   GJ158) from a Clontech human adult lung cDNA library.  Human
CC   TRAIN-R was also cloned from a second sequence subclone of a
CC   lambda gt10 cDNA (GJ156, see X24979).  Human TRAIN-R is expressed
CC   at low levels in every tissue and cell line tested thus far, with
CC   higher expression detected in heart, prostate, ovary, testis,
CC   peripheral blood lymphocytes, thyroid and adrenal gland.
CC   Cell death can be induced by administering an agent capable of
CC   inhibiting the binding of TRAIN-R to its ligand.  A claimed method
CC   of treating, or reducing, the advancement, severity or effects of
CC   an immunological disease in a mammal comprises administering a
CC   pharmaceutical composition which comprises a TRAIN-R blocking agent,
CC   e.g. soluble TRAIN-R.  TRAIN-R can be fused to an immunoglobulin to
CC   produce a fusion protein which may be targeted to various sites.
CC   It can be used in binding assays, and to identify antagonists and
CC   agonists.  Anti-TRAIN-R antibodies can be used to reduce the
CC   severity of an immune response or to treat cancer.  TRAIN-R
CC   blocking agents can also be used to reduce the severity or effects
CC   of an immunological disease (all claimed).
XX
SQ   Sequence 2185 BP; 546 A; 551 C; 550 G; 538 T; 0 other;


  Query Match             85.3%;  Score 1276.4;  DB 20;  Length 2185;
  Best Local Similarity   99.5%;  Pred. No. 9.1e-260;
  Matches 1280;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy      7 gtagaactctccaacaataaatacatttgataagaaagatggctttaaaagtgctactag 66
          | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141 gaagaactctccaacaataaatacatttgataagaaagatggctttaaaagtgctactag 200

Qy     67 aacaagagaaaacgtttttcactcttttagtattactaggctatttgtcatgtaaagtga 126
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    201 aacaagagaaaacgtttttcactcttttagtattactaggctatttgtcatgtaaagtga 260

Qy    127 cttgtgaaacaggagactgtagacagcaagaattcagggatcggtctggaaactgtgttc 186
          |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    261 cttgtgaatcaggagactgtagacagcaagaattcagggatcggtctggaaactgtgttc 320

Qy    187 cctgcaaccagtgtgggccaggcatggagttgtctaaggaatgtggcttcggctatgggg 246
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    247 aggatgcacagtgtgtgacgtgccggctgcacaggttcaaggaggactggggcttccaga 306
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    381 aggatgcacagtgtgtgacgtgccggctgcacaggttcaaggaggactggggcttccaga 440

Qy    307 aatgcaagccctgtctggactgcgcagtggtgaaccgctttcagaaggcaaattgttcag 366
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    441 aatgcaagccctgtctggactgcgcagtggtgaaccgctttcagaaggcaaattgttcag 500

Qy    367 ccaccagtgatgccatctgcggggactgcttgccaggattttataggaagacgaaacttg 426
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    501 ccaccagtgatgccatctgcggggactgcttgccaggattttataggaagacgaaacttg 560

Qy    427 tcggctttcaagacatggagtgtgtgccttgtggagaccctcctcctccttacgaaccgc 486
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Db    561 tcggctttcaagacatggagtgtgtgccttgtggagaccctcctcctccttacgaaccgc 620

Qy    487 actgtgccagcaaggtcaacctcgtgaagatcgcgtccacggcctccagcccacgggaca 546
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Qy    547 cggcgctggctgccgttatctgcagcgctctggccaccgtcctgctggccctgctcatcc 606
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Db    741 tctgtgtcatctattgtaagagacagtttatggagaagaaacccagctggtctctgcggt 800

Qy    667 cacaggacattcagtacaacggctctgagctgtcgtgtcttgacagacctcagctccacg 726
Db    801 cgcaggacattcagtacaacggctctgagctgtcgtgttttgacagacctcagctccacg 860

Qy    727 aatatgcccacagagcctgctgccagtgccgccgtgactcagtgcagacctgcgggccgg 786
Db    861 aatatgcccacagagcctgctgccagtgccgccgtgactcagtgcagacctgcgggccgg 920

Qy    787 tgcgcttgctcccatccatgtgctgtgaggaggcctgcagccccaacccggcgactcttg 846
Db    921 tgcgcttgctcccatccatgtgctgtgaggaggcctgcagccccaacccggcgactcttg 980

Qy    847 gttgtggggtgcattctgcagccagtcttcaggcaagaaacgcaggcccagccggggaga 906
Db    981 gttgtggggtgcattctgcagccagtcttcaggcaagaaacgcaggcccagccggggaga 1040

Qy    907 tggtgccgactttcttcggatccctcacgcagtccatctgtggcgagttttcagatgcct 966
Db   1041 tggtgccgactttcttcggatccctcacgcagtccatctgtggcgagttttcagatgcct 1100

Qy    967 ggcctctgatgcagaatcccatgggtggtgacaacatctctttttgtgactcttatcctg 1026
Db   1101 ggcctctgatgcagaatcccatgggtggtgacaacatctctttttgtgactcttatcctg 1160

Qy   1027 aactcactggagaagacattcattctctcaatccagaacttgaaagctcaacgtctttgg 1086
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Qy   1087 attcaaatagcagtcaagatttggttggtggggctgttccagtccagtctcattctgaaa 1146
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Qy   1147 actttacagcagctactgatttatctagatataacaacacactggtagaatcagcatcaa 1206
Db   1281 actttacagcagctactgatttatctagatataacaacacactggtagaatcagcatcaa 1340

Qy   1207 ctcaggatgcactaactatgagaagccagctagatcaggagagtggcgctatcatccacc 1266
Db   1341 ctcaggatgcactaactatgagaagccagctagatcaggagagtggcgctgtcatccacc 1400

Qy   1267 cagccactcagacgtccctccaggta 1292
Db   1401 cagccactcagacgtccctccaggaa 1426
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RESULT 6
X59346
ID X59346 standard; cDNA; 987 BP.
XX
AC X59346;
XX
DT 20-SEP-1999 (first entry)
XX
DE Human NTR-5 cDNA.
XX
KW NTR-5; human; receptor; signal transduction; bone; muscle;
KW diagnosis; therapy; ss.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
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FT		/*tag= a
FT	mat_peptide	58..987
FT		/*tag= b

XX

PN WO9933967-A2.
XX
PD 08-JUL-1999.
XX
PF 28-DEC-1998; 98WO-US27688.
XX
PR 29-DEC-1997; 97US-0068925.
XX
PA (REGE-) REGENERON PHARM INC.
XX
PI Valenzuela DM;
XX
DR WPI; 1999-419102/35.
DR P-PSDB; Y06400.
XX
PT New mammalian receptor NTR-5 polypeptides
XX
PS Claim 2a; Page 21-22; 27pp; English.
XX
CC This is the claimed coding region of human cDNA encoding a novel
CC receptor, designated NTR-5 (see Y06400), that shows homology to
CC osteoprotegerin and tumour necrosis factor receptor. The cDNA was
CC isolated from a heart cDNA library using mouse NTR-5 cDNA (see
CC X59345) as probe. Homology to osteoprotegerin suggests that NTR-5
CC is involved in the regulation of bone mass, and may be useful for
CC regulating development, proliferation and death of osteoblast or
CC osteoclast cells or for regulating muscle metabolism, and that it
CC may be implicated in muscle diseases or disorders. A host-vector
CC system for production of NTR-5 is claimed. NTR-5 polypeptides can
CC be used as immunogens and in screening assays to identify NTR-5
CC ligands, agonists and antagonists. The NTR-5 polynucleotide is
CC useful as a diagnostic tool, and as a source of probes and primers.
CC The invention also provides for diagnostic and therapeutic methods
CC based on the interaction of NTR-5 and agents that initiate signal
CC transduction through binding to NTR-5.
XX
SQ Sequence 987 BP; 220 A; 251 C; 278 G; 238 T; 0 other;

Query Match 55.9%; Score 835.6; DB 20; Length 987;
Best Local Similarity 99.5%; Pred. No. 4e-167;
Matches 838; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db      1 atggctttaaaagtgctactagaacaagagaaaacgtttttcactcttttagtattacta 60

Qy    105 ggctatttgtcatgtaaagtgacttgtgaaacaggagactgtagacagcaagaattcagg 164
Db     61 ggctatttgtcatgtaaagtgacttgtgaatcaggagactgtagacagcaagaattcagg 120

Qy    165 gatcggtctggaaactgtgttccctgcaaccagtgtgggccaggcatggagttgtctaag 224
Db    121 gatcggtctggaaactgtgttccctgcaaccagtgtgggccaggcatggagttgtctaag 180

Qy    225 gaatgtggcttcggctatggggaggatgcacagtgtgtgacgtgccggctgcacaggttc 284
Db    181 gaatgtggcttcggctatggggaggatgcacagtgtgtgacgtgccggctgcacaggttc 240

Qy    285 aaggaggactggggcttccagaaatgcaagccctgtctggactgcgcagtggtgaaccgc 344
Db    241 aaggaggactggggcttccagaaatgcaagccctgtctggactgcgcagtggtgaaccgc 300

Qy    345 tttcagaaggcaaattgttcagccaccagtgatgccatctgcggggactgcttgccagga 404
Db    301 tttcagaaggcaaattgttcagccaccagtgatgccatctgcggggactgcttgccagga 360

Qy    405 ttttataggaagacgaaacttgtcggctttcaagacatggagtgtgtgccttgtggagac 464
Db    361 ttttataggaagacgaaacttgtcggctttcaagacatggagtgtgtgccttgtggagac 420

Qy    465 cctcctcctccttacgaaccgcactgtgccagcaaggtcaacctcgtgaagatcgcgtcc 524
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Db    421 cctcctcctccttacgaaccgcactgtgccagcaaggtcaacctcgtgaagatcgcgtcc 480

Qy    525 acggcctccagcccacgggacacggcgctggctgccgttatctgcagcgctctggccacc 584
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 acggcctccagcccacgggacacggcgctggctgccgttatctgcagcgctctggccacc 540

Qy    585 gtcctgctggccctgctcatcctctgtgtcatctattgtaagagacagtttatggagaaag 644
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 gtcctgctggccctgctcatcctctgtgtcatctattgtaagagacagtttatggagaaag 600

Qy    645 aaacccagctggtctctgcggtcacaggacattcagtacaacggctctgagctgtcgtgt 704
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db    601 aaacccagctggtctctgcggtcgcaggacattcagtacaacggctctgagctgtcgtgt 660

Qy    705 cttgacagacctcagctccacgaatatgcccacagagcctgctgccagtgccgccgtgac 764
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Db    661 tttgacagacctcagctccacgaatatgcccacagagcctgctgccagtgccgccgtgac 720

Qy    765 tcagtgcagacctgcgggccggtgcgcttgctcccatccatgtgctgtgaggaggcctgc 824
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 tcagtgcagacctgcgggccggtgcgcttgctcccatccatgtgctgtgaggaggcctgc 780

Qy    825 agccccaacccggcgactcttggttgtggggtgcattctgcagccagtcttcaggcaaga 884
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Qy    885 aa 886
          ||
Db    841 aa 842
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RESULT   7
X23413
ID   X23413 standard; DNA; 1678 BP.
XX
AC   X23413;
XX
DT   18-JUN-1999  (first entry)
XX
DE   Mouse mAPO4-alpha (long) DNA.
XX
KW   Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
KW   developmental abnormality; gestational abnormalitity; prostate cancer;
KW   APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
KW   cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
KW   apoptosis; mouse; mAPO4-alpha; ss.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             72..1322
FT                   /*tag= a
FT                   /product= "mAPO4-alpha"
XX
PN   WO9911791-A2.
XX
PD   11-MAR-1999.
XX
PF   04-SEP-1998;   98WO-US18393.
XX
PR   05-SEP-1997;   97US-0924634.
XX
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Chaudhary PM;
XX
DR   WPI; 1999-205191/17.
DR   P-PSDB; W93579.
XX
PT   New Tumor Necrosis Factor family receptor polypeptides and ligands -
PT   useful for diagnosis and treatment of prostate cancer and
PT   developmental or gestational abnormalities
XX
PS   Example IV; Fig 7A; 156pp; English.
XX
CC   This invention describes isolated Tumor Necrosis Factor (TNF) family
CC   receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
CC   fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
CC   their active fragments. APO4 is useful for diagnosing prostate cancer
CC   by determining levels of APO4 in an individual. Prostate cancer can also
CC   be treated using APO4 selective binding agents linked to a therapeutic
CC   moiety. APO4 polypeptides are also useful for identifying selective
CC   binding agents, useful in diagnosis/treatment of disease by binding of
CC   agents to the polypeptide/active fragment which is extracellular, or
CC   expressed on the cell surface. The binding is preferably performed in
CC   vivo. APO4 polypeptides/ active fragments are also useful for screening
CC   for agonists and antagonists by binding and observing the changer in APO4
CC   activity. Effective pharmacological agents useful in diagnosis or
CC   treatment of disease are also identified using APO4 polypeptides/active
CC   fragments and APO4 signal transducer molecules that specifically interact
CC   with a cytoplasmic domain of APO4 and detecting a change in level of APO4
CC   activity. The method is performed in vivo or in vitro. APO polypeptides
CC   are all useful as immunogens for preparing antibodies. APO4 is also
CC   useful for diagnosis/treatment of developmental or gestational
CC   abnormalities. APO8 was transfected to human breast carcinoma cell line
CC   MCF-7, and induced apoptosis.
XX
SQ   Sequence 1678 BP; 371 A; 467 C; 466 G; 374 T; 0 other;
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  Query Match             49.5%;  Score 741;  DB 20;  Length 1678;
  Best Local Similarity   74.5%;  Pred. No. 3.7e-147;
  Matches  946;  Conservative    0;  Mismatches  320;  Indels    3;  Gaps    1;

Qy     22 aataaatacatttgataagaaagatggctttaaaagtgctactagaacaagagaaaacgt 81
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Db     49 aataaacacgtttggtgagagccatggcactcaaggtcctacctctacacaggacggtgc 108

Qy     82 ttttcactcttttagtattactaggctatttgtcatgtaaagtgacttgtgaaacaggag 141
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Db    109 tcttcgctgccattctcttcctactccacctggcatgtaaagtgagttgcgaaaccggag 168

Qy    142 actgtagacagcaagaattcagggatcggtctggaaactgtgttccctgcaaccagtgtg 201
          | || || ||||| ||||||| |||||| |||||||||||||| | |||||| ||||| |
Db    169 attgcaggcagcaggaattcaaggatcgatctggaaactgtgtcctctgcaaacagtgcg 228

Qy    202 ggccaggcatggagttgtctaaggaatgtggcttcggctatggggaggatgcacagtgtg 261
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Qy    262 tgacgtgccggctgcacaggttcaaggaggactggggcttccagaaatgcaagccctgtc 321
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Db    289 tgccctgcaggccgcaccggttcaaggaagactggggtttccagaagtgtaagccatgtg 348

Qy    322 tggactgcgcagtggtgaaccgctttcagaaggcaaattgttcagccaccagtgatgcca 381
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Qy    382 tctgcggggactgcttgccaggattttataggaagacgaaacttgtcggctttcaagaca 441
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Qy    442 tggagtgtgtgccttgtggagaccctcctcctccttacgaaccgcactgtgccagcaagg 501
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Qy    562 ttatctgcagcgctctggccaccgtcctgctggccctgctcatcctctgtgtcatctatt 621
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Qy    742 cctgctgccagtgccgccgtgactcagtgcagacctgcgggccggtgcgcttgctcccat 801
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Qy    802 ccatgtgctgtgaggaggcctgcagccccaacccggcgactcttggttgtggggtgcatt 861
          || |||||||||| |||||| ||||| |   ||  ||    ||||| |||||| ||| ||
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Qy    862 ctgcagccagtcttcaggcaagaaacgcaggcccagccggggagatggtgccgactttct 921
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Qy    922 tcggatccctcacgcagtccatctgtggcgagttttcagatgcctggcctctgatgcaga 981
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Qy    982 atcccatgggtggtgacaacatctctttttgtgactcttatcctgaactcactggagaag 1041
          ||||  |||| ||||   ||| |||| | ||||||||||||||||||||||||||||||
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Qy   1042 acattcattctctcaatccagaacttgaaagctcaacgtctttggattcaaatagcagtc 1101
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Qy   1102 aagatttggttggtggggctgttccagtccagtctcattctgaaaactttacagcagcta 1161
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Qy   1162 ctgatttatctagatataacaacacactggtagaatcagcatcaactcaggatgcactaa 1221
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Qy   1222 ctatgagaagccagctagatcaggagagtggcgctatcatccacccagccactcagacgt 1281
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Qy   1282 ccctccagg 1290
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Db   1306 ccttccagg 1314
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```
RESULT   8
X23414
ID   X23414 standard; DNA; 886 BP.
XX
AC   X23414;
XX
DT   18-JUN-1999  (first entry)
XX
DE   Mouse mAPO4-alpha (short) DNA.
XX
KW   Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
KW   developmental abnormality; gestational abnormalitity; prostate cancer;
KW   APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
KW   cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
KW   apoptosis; mouse; mAPO4-alpha; ss.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
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XX
PN   WO9911791-A2.
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PD   11-MAR-1999.
XX
PF   04-SEP-1998;   98WO-US18393.
XX
PR   05-SEP-1997;   97US-0924634.
XX
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Chaudhary PM;
XX
DR   WPI; 1999-205191/17.
DR   P-PSDB; W93580.
XX
PT   New Tumor Necrosis Factor family receptor polypeptides and ligands -
PT   useful for diagnosis and treatment of prostate cancer and
PT   developmental or gestational abnormalities
XX
PS   Example IV; Fig 7B; 156pp; English.
XX
CC   This invention describes isolated Tumor Necrosis Factor (TNF) family
CC   receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
CC   fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
CC   their active fragments. APO4 is useful for diagnosing prostate cancer
CC   by determining levels of APO4 in an individual. Prostate cancer can also
CC   be treated using APO4 selective binding agents linked to a therapeutic
CC   moiety. APO4 polypeptides are also useful for identifying selective
CC   binding agents, useful in diagnosis/treatment of disease by binding of
CC   agents to the polypeptide/active fragment which is extracellular, or
CC   expressed on the cell surface. The binding is preferably performed in
CC   vivo. APO4 polypeptides/ active fragments are also useful for screening
CC   for agonists and antagonists by binding and observing the changer in APO4
CC   activity. Effective pharmacological agents useful in diagnosis or
CC   treatment of disease are also identified using APO4 polypeptides/active
CC   fragments and APO4 signal transducer molecules that specifically interact
CC   with a cytoplasmic domain of APO4 and detecting a change in level of APO4
CC   activity. The method is performed in vivo or in vitro. APO polypeptides
CC   are all useful as immunogens for preparing antibodies. APO4 is also
CC   useful for diagnosis/treatment of developmental or gestational
CC   abnormalities. APO8 was transfected to human breast carcinoma cell line
CC   MCF-7, and induced apoptosis.
XX
SQ   Sequence 886 BP; 204 A; 245 C; 247 G; 190 T; 0 other;
```

```
  Query Match             30.8%;  Score 460.8;  DB 20;  Length 886;
  Best Local Similarity   81.9%;  Pred. No. 2.8e-88;
  Matches  531;  Conservative    0;  Mismatches  117;  Indels    0;  Gaps    0;

Qy     22 aataaatacatttgataagaaagatggctttaaaagtgctactagaacaagagaaaacgt 81
          |||||| || |||| | |||   |||||  | || || ||||    |||   ||    |
Db     49 aataaacacgtttggtgagagccatggcactcaaggtcctacctctacacaggacggtgc 108

Qy     82 ttttcactcttttagtattactaggctatttgtcatgtaaagtgacttgtgaaacaggag 141
          | ||| ||    |  | || |||  | |  || ||||||||||| ||| ||||| ||||
Db    109 tcttcgctgccattctcttcctactccacctggcatgtaaagtgagttgcgaaaccggag 168

Qy    142 actgtagacagcaagaattcagggatcggtctggaaactgtgttccctgcaaccagtgtg 201
          | || || ||||| ||||||| |||||| |||||||||||||| | |||||| ||||| |
Db    169 attgcaggcagcaggaattcaaggatcgatctggaaactgtgtcctctgcaaacagtgcg 228

Qy    202 ggccaggcatggagttgtctaaggaatgtggcttcggctatggggaggatgcacagtgtg 261
          | || |||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    229 gacctggcatggagttgtccaaggaatgtggcttcggctatggggaggatgcacagtgtg 288

Qy    262 tgacgtgccggctgcacaggttcaaggaggactggggcttccagaaatgcaagccctgtc 321
          || | ||| ||| |||| |||||||||| |||||||| |||||||| || ||||| |||
Db    289 tgccctgcaggccgcaccggttcaaggaagactgggggtttccagaagtgtaagccatgtg 348

Qy    322 tggactgcgcagtggtgaaccgctttcagaaggcaaattgttcagccaccagtgatgcca 381
           |||||| ||  |||||||||||||||||| ||| || || |||  ||||||||||||
Db    349 cggactgtgcgctggtgaaccgctttcagagggccaactgctcacacaccagtgatgctg 408

Qy    382 tctgcggggactgcttgccaggatttttataggaagacgaaacttgtcggctttcaagaca 441
          |||||||||||||| ||||||||||||  ||||||| ||||| || || ||||||||||
```

```
Db    409 tctgcggggactgcctgccaggattttaccggaagaccaaactggttggttttcaagaca 468

Qy    442 tggagtgtgtgccttgtggagaccctcctcctcctcttacgaaccgcactgtgccagcaagg 501
          |||||||||||||| || |||||||| |||||||| |||||||| |||||| |||||||||
Db    469 tggagtgtgtgccctgcggagacccacctcctccctacgaaccacactgtaccagcaagg 528

Qy    502 tcaacctcgtgaagatcgcgtccacggcctccagcccacgggacacggcgctggctgccg 561
          | ||||| ||||||||| | ||||| | ||||||||| ||||||||||||||||||||
Db    529 tgaaccttgtgaagatctcctccaccgtctccagccctcgggacacggcgctggctgccg 588

Qy    562 ttatctgcagcgctctggccaccgtcctgctggccctgctcatcctctgtgtcatctatt 621
          | |||||||| |||||||||| || ||||| |||||||||||||| |||||||||| |
Db    589 tcatctgcagtgctctggccacggtgctgctcgccctgctcatcctgtgtgtcatctact 648

Qy    622 gtaagagacagtttatggagaagaaacccagctggtctctgcggtcac 669
          | ||||| ||||| ||||||||||||||||||||    || |  || |
Db    649 gcaagaggcagttcatggagaagaaacccagctgtaagctcccatccc 696


RESULT  9
X24977
ID   X24977 standard; cDNA; 942 BP.
XX
AC   X24977;
XX
DT   05-JUL-1999  (first entry)
XX
DE   Mouse TRAIN-R (long form) cDNA.
XX
KW   TRAIN-R; receptor; mouse; tumour necrosis factor receptor;
KW   agonist; antagonist; cancer; immunological disease; therapy;
KW   cytostatic; ss.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   CDS             101..745
FT                   /*tag= a
XX
PN   WO9913078-A1.
XX
PD   18-MAR-1999.
XX
PF   11-SEP-1998;   98WO-US19030.
XX
PR   06-MAY-1998;   98US-0084422.
PR   12-SEP-1997;   97US-0058631.
XX
PA   (BIOJ ) BIOGEN INC.
XX
PI   Hession C,  Tschopp J;
XX
DR   WPI; 1999-229238/19.
DR   P-PSDB; W98145.
XX
PT   New cysteine-rich tumor necrosis factor receptor
XX
PS   Claim 1; Page 26-27; 30pp; English.
XX
CC   The present sequence encodes a novel murine cysteine-rich tumour
CC   necrosis factor receptor family member termed TRAIN-R (long form)
CC   (see W98145).  Murine TRAIN-R is expressed at high levels in brain
CC   and lung, and at lower levels in liver, skeletal muscle and kidney.
CC   Cell death can be induced by administering an agent capable of
CC   inhibiting the binding of TRAIN-R to its ligand.  A claimed method
CC   of treating, or reducing, the advancement, severity or effects of
CC   an immunological disease in a mammal comprises administering a
CC   pharmaceutical composition which comprises a TRAIN-R blocking agent,
CC   e.g. soluble TRAIN-R (see also W98144).  TRAIN-R can be fused to an
CC   immunoglobulin molecule to produce a fusion protein which may be
CC   targeted to various sites.  It can be used in binding assays, and
CC   to identify antagonists and agonists.  Anti-TRAIN receptor
CC   antibodies can be used to reduce the severity of an immune response
CC   or to treat cancer.  TRAIN-R blocking agents can be used to reduce
CC   the severity or effects of an immunological disease (all claimed).
XX
SQ   Sequence 942 BP; 219 A; 264 C; 258 G; 200 T; 1 other;


  Query Match             30.8%;  Score 460.8;  DB 20;  Length 942;
  Best Local Similarity   81.9%;  Pred. No. 2.8e-88;
  Matches  531;  Conservative    0;  Mismatches  117;  Indels    0;  Gaps    0;

Qy      22 aataaatacatttgataagaaagatggctttaaaagtgctactagaacaagagaaaacgt 81
           |||||| || |||| | |||   |||||  | || || ||||    |||   ||     |
Db      78 aataaacacgtttggtgagagccatggcactcaaggtcctacctctacacaggacggtgc 137

Qy      82 ttttcactcttttagtattactaggctatttgtcatgtaaagtgacttgtgaaacaggag 141
           | ||| ||    |  | || |||  | |  || ||||||||||||| ||| ||||| ||||
Db     138 tcttcgctgccattctcttcctactccacctggcatgtaaagtgagttgcgaaaccggag 197

Qy     142 actgtagacagcaagaattcagggatcggtctggaaactgtgttccctgcaaccagtgtg 201
           | || || ||||| ||||||| |||||| |||||||||||||| | |||||| ||||| |
Db     198 attgcaggcagcaggaattcaaggatcgatctggaaactgtgtcctctgcaaacagtgcg 257

Qy     202 ggccaggcatggagttgtctaaggaatgtggcttcggctatggggaggatgcacagtgtg 261
           | || |||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db     258 gacctggcatggagttgtccaaggaatgtggcttcggctatggggaggatgcacagtgtg 317

Qy     262 tgacgtgccggctgcacaggttcaaggaggactggggcttccagaaatgcaagccctgtc 321
           || | ||| ||| |||| |||||||||| |||||||| |||||||| || ||||| |||
Db     318 tgccctgcaggccgcaccggttcaaggaagactggggtttccagaagtgtaagccatgtg 377

Qy     322 tggactgcgcagtggtgaaccgctttcagaaggcaaattgttcagccaccagtgatgcca 381
           ||||||  ||  |||||||||||||||||| ||| || || ||| ||||||||||||
Db     378 cggactgtgcgctggtgaaccgctttcagagggccaactgctcacacaccagtgatgctg 437

Qy     382 tctgcggggactgcttgccaggattttataggaagacgaaacttgtcggctttcaagaca 441
           |||||||||||||| |||||||||||||  ||||||| ||||| || || ||||||||||
Db     438 tctgcggggactgcctgccaggattttaccggaagaccaaactggttggttttcaagaca 497

Qy     442 tggagtgtgtgccttgtggagaccctcctcctcctcttacgaaccgcactgtgccagcaagg 501
           |||||||||||||| || |||||||| |||||||| |||||||| |||||| |||||||||
Db     498 tggagtgtgtgccctgcggagacccacctcctccctacgaaccacactgtaccagcaagg 557

Qy     502 tcaacctcgtgaagatcgcgtccacggcctccagcccacgggacacggcgctggctgccg 561
           | ||||| ||||||||| | ||||| | |||||||||| ||||||||||||||||||||
Db     558 tgaaccttgtgaagatctcctccaccgtctccagccctcgggacacggcgctggctgccg 617

Qy     562 ttatctgcagcgctctggccaccgtcctgctggccctgctcatcctctgtgtcatctatt 621
           | |||||||| |||||||||| || ||||| |||||||||||||| |||||||||| |
Db     618 tcatctgcagtgctctggccacggtgctgctcgccctgctcatcctgtgtgtcatctact 677

Qy     622 gtaagagacagtttatggagaagaaacccagctggtctctgcggtcac 669
           | ||||| ||||| ||||||||||||||||||||    || |  || |
Db     678 gcaagaggcagttcatggagaagaaacccagctgtaagctcccatccc 725


RESULT  10
X87394
ID   X87394 standard; cDNA; 981 BP.
XX
AC   X87394;
XX
DT   08-OCT-1999  (first entry)
XX
DE   Mouse STRIFE1 (Tango 127a) cDNA.
XX
KW   STRIFE1; Tango 127a; T127a; mouse; tumour necrosis factor receptor;
KW   sepsis; circulatory collapse; toxic shock; infection;
KW   immune disease; autoimmune disease; alcohol-induced hepatitis;
KW   inflammation; graft versus host pathology; cancer; tumour;
KW   cerebral malaria; multiple sclerosis; diagnosis; therapy; ss.
XX
OS   Mus musculus.
XX
```

```
FH   Key             Location/Qualifiers
FT   5'UTR           1..106
FT                   /*tag= a
FT                   /note= "an isolated nucleic acid molecule
FT                          comprising this region of the sequence is
FT                          specifically claimed in Claim 3"
FT   CDS             107..751
FT                   /*tag= b
FT                   /product= STRIFE1
FT                   /note= "an isolated nucleic acid molecule
FT                          comprising the coding region is
FT                          specifically claimed in Claim 2"
FT   sig_peptide     107..193
FT                   /*tag= c
FT   mat_peptide     194..748
FT                   /*tag= d
FT                   /note= "an isolated nucleic acid molecule
FT                          comprising the mature protein coding region
FT                          is specifically claimed in Claim 14"
FT   3'UTR           752..981
FT                   /*tag= e
FT                   /note= "an isolated nucleic acid molecule
FT                          comprising this region of the sequence is
FT                          specifically claimed in Claim 4 "
XX
PN   WO9937818-A1.
XX
PD   29-JUL-1999.
XX
PF   27-JAN-1999;   99WO-US01679.
XX
PR   27-JAN-1998;   98US-0014195.
XX
PA   (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
PI   Busfield SJ;
XX
DR   WPI; 1999-458707/38.
DR   P-PSDB; Y06522.
XX
PT   New STRIFEI and STRIFEII polypeptides, proteins and nucleic acid
PT   molecules useful for modulating TNFR associated disorders
XX
PS   Claim 3; Fig 1A-B; 119pp; English.
XX
CC   This is the nucleotide sequence of mouse STRIFE1 (also called
CC   Tango 127a or T127a) cDNA.  It encodes a protein (see Y05422) that
CC   belongs to the tumour necrosis factor receptor (TNFR) superfamily.
CC   2 Splice forms of murine STRIFE have been identified, one that is
CC   predicted to be membrane-bound (STRIFE1) and one that is secreted
CC   (STRIFE2, see Y06523).  STRIFE was identified as a TNFR homologue
CC   by a computer-based search of public EST databases.  The invention
CC   provides STRIFE1 and STRIFE2 polynucleotides and polypeptides, as
CC   well as fusion proteins, antigenic peptides and antibodies.  It
CC   also provides expression vectors, host cells and transgenic
CC   animals, as well as diagnostic, screening and therapeutic methods.
CC   STRIFE I and STRIFE II may play a role in mediating inflammatory,
CC   immune and host defense functions and may play a role in various
CC   neoplastic disease states.  They may be useful as targets for
CC   developing novel diagnostic and therapeutic agents for TNF- and
CC   TNFR-associated disorders.  Examples include sepsis syndrome,
CC   circulatory collapse and shock resulting from bacterial infection,
CC   acute and chronic parasitic or infectious processes, acute and
CC   chronic immune and autoimmune pathologies, alcohol-induced
CC   hepatitis, chronic inflammatory pathologies, vascular inflammatory
CC   pathologies, graft-versus-host pathology, malignant pathologies
CC   involving TNF-secreting tumors, cerebral malaria and multiple
CC   sclerosis.
XX
SQ   Sequence 981 BP; 247 A; 270 C; 264 G; 200 T; 0 other;

  Query Match             30.8%;  Score 460.8;  DB 20;  Length 981;
```

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  Best Local Similarity   81.9%;  Pred. No. 2.9e-88;
  Matches  531;  Conservative    0;  Mismatches  117;  Indels    0;  Gaps    0;

Qy      22 aataaatacatttgataagaaagatggctttaaaagtgctactagaacaagagaaaacgt 81
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Db      84 aataaacacgtttggtgagagccatggcactcaaggtcctacctctacacaggacggtgc 143

Qy      82 ttttcactcttttagtattactaggctatttgtcatgtaaagtgacttgtgaaacaggag 141
           | ||| ||    |  | || |||  | |  || ||||||||||||| ||| ||||| ||||
Db     144 tcttcgctgccattctcttcctactccacctggcatgtaaagtgagttgcgaaaccggag 203

Qy     142 actgtagacagcaagaattcagggatcggtctggaaactgtgttccctgcaaccagtgtg 201
           | || || ||||| ||||||| |||||| |||||||||||||| | |||||| ||||| |
Db     204 attgcaggcagcaggaattcaaggatcgatctggaaactgtgtcctctgcaaacagtgcg 263

Qy     202 ggccaggcatggagttgtctaaggaatgtggcttcggctatggggaggatgcacagtgtg 261
           | || |||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db     264 gacctggcatggagttgtccaaggaatgtggcttcggctatggggaggatgcacagtgtg 323

Qy     262 tgacgtgccggctgcacaggttcaaggaggactggggcttccagaaatgcaagccctgtc 321
           || | ||| ||| |||| |||||||||| |||||||| |||||||| || ||||| |||
Db     324 tgccctgcaggccgcaccggttcaaggaagactggggtttccagaagtgtaagccatgtg 383

Qy     322 tggactgcgcagtggtgaaccgctttcagaaggcaaattgttcagccaccagtgatgcca 381
           ||||||  ||  ||||||||||||||||||| ||| || || ||| ||||||||||||
Db     384 cggactgtgcgctggtgaaccgctttcagagggccaactgctcacacaccagtgatgctg 443

Qy     382 tctgcggggactgcttgccaggattttataggaagacgaaacttgtcggctttcaagaca 441
           |||||||||||||| ||||||||||||  |||||||  ||||| || || ||||||||||
Db     444 tctgcggggactgcctgccaggattttaccggaagaccaaactggttggttttcaagaca 503

Qy     442 tggagtgtgtgccttgtggagaccctcctcctcctcttacgaaccgcactgtgccagcaagg 501
           |||||||||||||  || |||||||| |||||||| |||||||| |||||| |||||||||
Db     504 tggagtgtgtgccctgcggagacccacctcctccctacgaaccacactgtaccagcaagg 563

Qy     502 tcaacctcgtgaagatcgcgtccacggcctccagcccacgggacacggcgctggctgccg 561
           | ||||| ||||||||| | ||||| | ||||||||| ||||||||||||||||||||||
Db     564 tgaaccttgtgaagatctcctccaccgtctccagccctcgggacacggcgctggctgccg 623

Qy     562 ttatctgcagcgctctggccaccgtcctgctggccctgctcatcctctgtgtcatctatt 621
           | |||||||| |||||||||| || ||||| |||||||||||||| |||||||||| |
Db     624 tcatctgcagtgctctggccacggtgctgctcgccctgctcatcctgtgtgtcatctact 683

Qy     622 gtaagagacagtttatggagaagaaacccagctggtctctgcggtcac 669
           | ||||| ||||| ||||||||||||||||||||    || |  || |
Db     684 gcaagaggcagttcatggagaagaaacccagctgtaagctcccatccc 731
```

```
RESULT  11
X84622
ID   X84622 standard; DNA; 893 BP.
XX
AC   X84622;
XX
DT   16-SEP-1999  (first entry)
XX
DE   Human TNFR superfamily soluble receptor coding sequence.
XX
KW   TNFL1; human; TNFR superfamily; tumour necrosis factor ligand; TNF;
KW   tumour necrosis factor receptor; TNFR superfamily; cell proliferation;
KW   cell differentiation; cytokine production; immunoglobulin; hyperplasia;
KW   apoptosis inducer; activated T cell; autoimmune disease; inhibitor;
KW   myasthenia gravis; insulin-dependent diabetes mellitus; endotoxic shock;
KW   rheumatoid.arthritis; multiple sclerosis; systemic lupus erythematosus;
KW   tumour; proliferative disorder; neoplasia; dysplasia; immunocompetence;
KW   lymphoid organogenesis; bacterial resistance; contact hypersensitivity;
KW   delayed type sensitivity; therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO9933980-A2.
XX
PD   08-JUL-1999.
```

XX
PF 22-DEC-1998; 98WO-US27474.
XX
PR 16-DEC-1998; 98US-0212270.
PR 30-DEC-1997; 97US-0068959.
XX
PA (CHIR) CHIRON CORP.
XX
PI Kassam A, Lamson G, Pot D, Tribouley C;
XX
DR WPI; 1999-405508/34.
DR P-PSDB; Y22223.
XX
PT New tumour necrosis factor ligands, useful for induction of cell
PT death and/or proliferation of cells
XX
PS Claim 15; Page 65-66; 69pp; English.
XX
CC This sequence encodes a tumour necrosis factor receptor (TNFR)
CC superfamily soluble protein of the invention. The invention also relates
CC to tumour necrosis factor (TNF) ligand (TNFL) family proteins. The TNFL
CC proteins play regulatory roles in cell proliferation and/or
CC differentiation, e.g. they can induce production of cytokines,
CC immunoglobulins, etc. A variety of diseases can be treated by modulating
CC the activity of TNFL proteins, e.g. they can induce apoptosis of
CC activated T cells but rescue resting T cell from apoptosis. TNFL
CC polypeptides can therefore be used to treat autoimmune diseases, such as
CC myasthenia gravis, insulin-dependent diabetes mellitus, rheumatoid
CC arthritis, multiple sclerosis, and systemic lupus erythematosus. TNFL
CC proteins also have tumour stimulating properties, so tumours can be
CC treated by inhibiting the expression or activity of TNFL. Other
CC proliferative disorders, such as neoplasias, dysplasias, and hyperplasia
CC can also be treated using TNFL inhibitors. The TNFL polypeptides and
CC polynucleotides can also be used to enhance or decrease TNF activity,
CC thus providing therapeutic benefits such as induction of cell death,
CC lymphoid organogenesis, or host bacterial resistance, and inhibition of
CC endotoxic shock, contact hypersensitivity, delayed type sensitivity or
CC immunocompetence of a transplant recipient. TNF and its receptors play a
CC major role in host defence and immunosurveillance. As such, there is a
CC need to identify new members of TNFR families. This invention provides
CC this need.
XX
SQ Sequence 893 BP; 211 A; 240 C; 247 G; 195 T; 0 other;

Query Match 29.9%; Score 447.2; DB 20; Length 893;
Best Local Similarity 81.6%; Pred. No. 2e-85;
Matches 529; Conservative 0; Mismatches 118; Indels 1; Gaps 1;

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Qy     22 aataaatacatttgataagaaagatggctttaaaagtgctactagaacaagagaaaacgt 81
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Db     32 aataaacacgtttggtgagagccatggcactcaaggtcctacctctacacaggacggtgc 91

Qy     82 ttttcactcttttagtattactaggctatttgtcatgtaaagtgacttgtgaaacaggag 141
          | ||| ||    |  | || |||  | |  || ||||||||||||| ||| ||||| ||||
Db     92 tcttcgctgccattctcttcctactccacctggcatgtaaagtgagttgcgaaaccggag 151

Qy    142 actgtagacagcaagaattcagggatcggtctggaaactgtgttccctgcaaccagtgtg 201
          | || || ||||| ||||||| |||||| |||||||||||||| | |||||| ||||| |
Db    152 attgcaggcagcaggaattcaaggatcgatctggaaactgtgtcctctgcaaacagtgcg 211

Qy    202 ggccaggcatggagttgtctaaggaatgtggcttcggctatggggaggatgcacagtgtg 261
          | || |||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db    212 gacctggcatggagttgtccaaggaatgtggcttcggctatggggaggatgcacagtgtg 271

Qy    262 tgacgtgccggctgcacaggttcaaggaggactggggcttccagaaatgcaagccctgtc 321
          || | ||| ||| |||| |||||||||| |||||||| |||||||| || ||||| |||
Db    272 tgccctgcaggccgcaccggttcaaggaagactggggtttccagaagtgtaagccatgtg 331

Qy    322 tggactgcgcagtggtgaaccgctttcagaaggcaaattgttcagccaccagtgatgcca 381
          |||||| ||  |||||||||||||||| ||| || || |||  ||||||||||
Db    332 cggactgtgcgctggtgaaccgctttcagagggccaactgctcacacaccagtgatgctg 391

Qy    382 tctgcggggactgcttgccaggattttataggaagacgaaacttgtcggctttcaagaca 441
          |||||||||||||| |||||||||||||  ||||||| ||||| || || ||||||||||
Db    392 tctgcggggactgcctgccaggattttaccggaagaccaaactggttggttttcaagaca 451

Qy    442 tggagtgtgtgccttgtggagaccctcctcctccttacgaaccgcactgtgccagcaagg 501
          |||||||||||||| || |||||||| |||||||| |||||||| |||||| |||||||||
Db    452 tggagtgtgtgccctgcggagacccacctcctccctacgaaccacactgtaccagcaagg 511

Qy    502 tcaacctcgtgaagatcgcgtccacggcctccagcccacgggacacggcgctggctgccg 561
          | ||||| ||||||||| | ||||| | |||||||| |||||||||||| |||||||||
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Qy    562 ttatctgcagcgctctggccaccgtcctgctggccctgctcatcctctgtgtcatctatt 621
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Db    572 tcatctgcagtgctctggccacggtgctgctcg-cctgctcatcctgtgtgtcatctact 630

Qy    622 gtaagagacagtttatggagaagaaacccagctggtctctgcggtcac 669
          | ||||| ||||| ||||||||||||||||||||    || |  || |
Db    631 gcaagaggcagttcatggagaagaaacccagctgtaagctcccatccc 678
```

RESULT 12
X59345
ID X59345 standard; cDNA; 538 BP.
XX
AC X59345;
XX
DT 20-SEP-1999 (first entry)
XX
DE Mouse NTR-5 cDNA.
XX
KW NTR-5; mouse; receptor; signal transduction; bone; muscle;
KW diagnosis; therapy; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 3..485
FT /*tag= a
XX
PN WO9933967-A2.
XX
PD 08-JUL-1999.
XX
PF 28-DEC-1998; 98WO-US27688.
XX
PR 29-DEC-1997; 97US-0068925.
XX
PA (REGE-) REGENERON PHARM INC.
XX
PI Valenzuela DM;
XX
DR WPI; 1999-419102/35.
DR P-PSDB; Y06399.
XX
PT New mammalian receptor NTR-5 polypeptides
XX
PS Example 1; Page 19; 27pp; English.
XX
CC This is the nucleotide sequence of murine cDNA coding for a novel
CC receptor, designated NTR-5 (see Y06399), that shows homology to
CC osteoprotegerin and tumour necrosis factor (TNF) receptor. 2 cDNA
CC clones containing the present sequence were isolated following an
CC EST database search using human and mouse TNF family members as
CC query sequences. The murine NTR-5 cDNA was used as a probe in
CC the isolation of human NTR-5 cDNA (see X59346). Homology to
CC osteoprotegerin suggests that NTR-5 is involved in the regulation
CC of bone mass, and may be useful for regulating development,
CC proliferation and death of osteoblast or osteoclast cells or for
CC regulating muscle metabolism, and that it may be implicated in
CC muscle diseases or disorders. A host-vector system for production
CC of NTR-5 is claimed. NTR-5 polypeptides can be used as immunogens
CC and in screening assays to identify NTR-5 ligands, agonists and

```
CC   antagonists.  The NTR-5 polynucleotide is useful as a diagnostic
CC   tool, and as a source of probes and primers.  The invention also
CC   provides for diagnostic and therapeutic methods based on the
CC   interaction of NTR-5 and agents that initiate signal transduction
CC   through binding to NTR-5.
XX
SQ   Sequence 538 BP; 111 A; 153 C; 152 G; 122 T; 0 other;


  Query Match             24.2%;  Score 362.6;  DB 20;  Length 538;
  Best Local Similarity   86.2%;  Pred. No. 1.1e-67;
  Matches  401;  Conservative    0;  Mismatches   64;  Indels    0;  Gaps    0;

Qy     205 caggcatggagttgtctaaggaatgtggcttcggctatggggaggatgcacagtgtgtga 264
           | ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1 ctggcatggagttgtccaaggaatgtggcttcggctatggggaggatgcacagtgtgtgc 60

Qy     265 cgtgccggctgcacaggttcaaggaggactggggcttccagaaatgcaagccctgtctgg 324
           | ||| ||| |||| |||||||||| |||||||| |||||||| || ||||| |||  ||
Db      61 cctgcaggccgcaccggttcaaggaagactggggtttccagaagtgtaagccatgtgcgg 120

Qy     325 actgcgcagtggtgaaccgctttcagaaggcaaattgttcagccaccagtgatgccatct 384
           |||| ||  |||||||||||||||||| ||| || || ||| ||||||||||  |||
Db     121 actgtgcgctggtgaaccgctttcagagggccaactgctcacacaccagtgatgctgtct 180

Qy     385 gcggggactgcttgccaggattttataggaagacgaaacttgtcggctttcaagacatgg 444
           |||||||||| |||||||||||  ||||||| ||||| || || ||||||||||||
Db     181 gcggggactgcctgccaggattttaccggaagaccaaactggttggttttcaagacatgg 240

Qy     445 agtgtgtgccttgtggagaccctcctcctccttacgaaccgcactgtgccagcaaggtca 504
           |||||||||| || |||||||| |||||||| |||||||| |||||| |||||||||| |
Db     241 agtgtgtgccctgcggagacccacctcctccctacgaaccacactgtaccagcaaggtga 300

Qy     505 acctcgtgaagatcgcgtccacggcctccagcccacgggacacggcgctggctgccgtta 564
           |||| ||||||||  | ||||| | |||||||||| ||||||||||||||||||||| |
Db     301 accttgtgaagatttcctccaccgtctccagccctcgggacacggcgctggctgccgtca 360

Qy     565 tctgcagcgctctggccaccgtcctgctggccctgctcatcctctgtgtcatctattgta 624
           ||||||| |||||||||| || ||||| |||||||||||||| |||||||||| || |
Db     361 tctgcagtgctctggccacggtgctgctcgccctgctcatcctgtgtgtcatctactgca 420

Qy     625 agagacagtttatggagaagaaacccagctggtctctgcggtcac 669
           |||| ||||| ||||||||||||||||||||    || |  || |
Db     421 agaggcagttcatggagaagaaacccagctgtaagctcccatccc 465


RESULT  13
V11422
ID   V11422 standard; cDNA; 371 BP.
XX
AC   V11422;
XX
DT   23-JUL-1998  (first entry)
XX
DE   Human secreted protein clone AX92_3 cDNA 5'-end.
XX
KW   Secreted protein; prevention; treatment; gene therapy; ds.
XX
OS   Homo sapiens.
XX
PN   WO9801554-A2.
XX
PD   15-JAN-1998.
XX
PF   07-JUL-1997;   97WO-US11876.
XX
PR   09-JUL-1996;   96US-0677231.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Bowman M,  Evans C,  Jacobs K,  LaVallie ER,  McCoy JM;
PI   Merberg D,  Racie LA,  Spaulding V,  Treacy M;
XX
DR   WPI; 1998-110230/10.
DR   P-PSDB; W58844.
XX
PT   Secreted proteins and polynucleotides encoding them - useful to
PT   prevent, treat and ameliorate medical conditions
XX
PS   Claim 15; Page 57; 93pp; English.
XX
CC   V11422-V11424 encode fragments of a novel secreted protein derived from
CC   clone AX92_3 which was isolated from a human adult testes cDNA library.
CC   The protein can be used to prevent, treat or ameliorate a medical
CC   condition, while the polynucleotides can be used for gene therapy.
XX
SQ   Sequence 371 BP; 83 A; 96 C; 107 G; 82 T; 3 other;


  Query Match             24.2%;  Score 361.6;  DB 19;  Length 371;
  Best Local Similarity   98.1%;  Pred. No. 1.6e-67;
  Matches  364;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy     172 ctggaaactgtgttccctgcaaccagtgtgggccaggcatggagttgtctaaggaatgtg 231
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Db       1 ctggaaactgtgttccctgcaaccagtgtgggccaggcatggagttgtctaaggaatgtg 60

Qy     232 gcttcggctatggggaggatgcacagtgtgtgacgtgccggctgcacaggttcaaggagg 291
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 gcttcggctatggggaggatgcacagtgtgtgacgtgccggctgcacaggttcaaggagg 120

Qy     292 actggggcttccagaaatgcaagccctgtctggactgcgcagtggtgaaccgctttcaga 351
           |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db     121 actggggcttccaaaaatgcaagccctgtctggactgcgcagtggtgaaccgctttcaga 180

Qy     352 aggcaaattgttcagccaccagtgatgccatctgcggggactgcttgccaggattttata 411
           |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db     181 aggcaaattgttcagccaccagtgatgccatctgcggggactgcttgccangattttata 240

Qy     412 ggaagacgaaacttgtcggctttcaagacatggagtgtgtgccttgtggagaccctcctc 471
           ||||||| |||||||||||||||||| |||||||||||||||||||||||| |||||||||
Db     241 ggaagacnaaacttgtcggctttcaaaacatggagtgtgtgccttgtggaaaccctcctc 300

Qy     472 ctccttacgaaccgcactgtgccagcaaggtcaacctcgtgaagatcgcgtccacggcct 531
           |||||||||||||||||||||||||||||||||||||||||| ||| ||||||||||||
Db     301 ctccttacgaaccgcactgtgccagcaaggtcaacctcgtgaaaatcncgtccacggcct 360

Qy     532 ccagcccacgg 542
           ||||||||||||
Db     361 ccagcccacgg 371


RESULT  14
X23417
ID   X23417 standard; DNA; 591 BP.
XX
AC   X23417;
XX
DT   18-JUN-1999  (first entry)
XX
DE   Mouse mAPO4-gamma DNA.
XX
KW   Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
KW   developmental abnormality; gestational abnormalitity; prostate cancer;
KW   APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
KW   cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
KW   apoptosis; mouse; APO4-gamma; ss.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             95..547
FT                   /*tag=  a
FT                   /product= "mAPO4-gamma"
XX
PN   WO9911791-A2.
```

XX
PD 11-MAR-1999.
XX
PF 04-SEP-1998; 98WO-US18393.
XX
PR 05-SEP-1997; 97US-0924634.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Chaudhary PM;
XX
DR WPI; 1999-205191/17.
DR P-PSDB; W93583.
XX
PT New Tumor Necrosis Factor family receptor polypeptides and ligands -
PT useful for diagnosis and treatment of prostate cancer and
PT developmental or gestational abnormalities
XX
PS Disclosure; Fig 7E; 156pp; English.
XX
CC This invention describes isolated Tumor Necrosis Factor (TNF) family
CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
CC their active fragments. APO4 is useful for diagnosing prostate cancer
CC by determining levels of APO4 in an individual. Prostate cancer can also
CC be treated using APO4 selective binding agents linked to a therapeutic
CC moiety. APO4 polypeptides are also useful for identifying selective
CC binding agents, useful in diagnosis/treatment of disease by binding of
CC agents to the polypeptide/active fragment which is extracellular, or
CC expressed on the cell surface. The binding is preferably performed in
CC vivo. APO4 polypeptides/ active fragments are also useful for screening
CC for agonists and antagonists by binding and observing the changer in APO4
CC activity. Effective pharmacological agents useful in diagnosis or
CC treatment of disease are also identified using APO4 polypeptides/active
CC fragments and APO4 signal transducer molecules that specifically interact
CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4
CC activity. The method is performed in vivo or in vitro. APO polypeptides
CC are all useful as immunogens for preparing antibodies. APO4 is also
CC useful for diagnosis/treatment of developmental or gestational
CC abnormalities. APO8 was transfected to human breast carcinoma cell line
CC MCF-7, and induced apoptosis.
XX
SQ Sequence 591 BP; 148 A; 145 C; 175 G; 123 T; 0 other;

Query Match 21.8%; Score 326.6; DB 20; Length 591;
Best Local Similarity 78.2%; Pred. No. 4.3e-60;
Matches 392; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

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Db     68 caggaataaacacgtttggtgagagccatggcactcaaggtcctacctctacacaggacg 127

Qy     78 acgtttttcactcttttagtattactaggctatttgtcatgtaaagtgacttgtgaaaca 137
            | | ||| ||    |  | || |||  | |  || ||||||||||||| ||| |||||
Db    128 gtgctcttcgctgccattctcttcctactccacctggcatgtaaagtgagttgcgaaacc 187

Qy    138 ggagactgtagacagcaagaattcagggatcggtctggaaactgtgttccctgcaaccag 197
          ||||| || || ||||| |||||||  ||||||  |||||||||||||| | ||||||  |||
Db    188 ggagattgcaggcagcaggaattcaaggatcgatctggaaactgtgtcctctgcaaacag 247

Qy    198 tgtgggccaggcatggagttgtctaaggaatgtggcttcggctatggggaggatgcacag 257
          || || || |||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    248 tgcggacctggcatggagttgtccaaggaatgtggcttcggctatggggaggatgcacag 307

Qy    258 tgtgtgacgtgccggctgcacaggttcaaggaggactggggcttccagaaatgcaagccc 317
          ||||||  | ||| ||| |||| |||||||||| ||||||||  |||||||| || |||||
Db    308 tgtgtgccctgcaggccgcaccggttcaaggaagactggggtttccagaagtgtaagcca 367

Qy    318 tgtctggactgcgcagtggtgaaccgctttcagaaggcaaattgttcagccaccagtgat 377
          |||  |||||| ||  |||||||||||||||||| ||| || || |||  ||||||||||
Db    368 tgtgcggactgtgcgctggtgaaccgctttcagagggccaactgctcacacaccagtgat 427
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Qy    378 gccatctgcggggactgcttgccaggattttataggaagacgaaacttgtcggctttcaa 437
          ||  |||||||||||||| ||||||||||||  ||||||| ||||| || || ||||||
Db    428 gctgtctgcggggactgcctgccaggattttaccggaagaccaaactggttggttttcaa 487

Qy    438 gacatggagtgtgtgccttgtggagaccctcctcctccttacgaaccgcactgtgccagc 497
          ||||||||||||||||| || |||||||| |||||||| |||||||| |||||||   |
Db    488 gacatggagtgtgtgccctgcggagacccacctcctccctacgaaccacactgtgagtga 547

Qy    498 aaggtcaacctcgtgaagatc 518
             | |||      | ||| |
Db    548 tgtgccaagtggcagcagacc 568
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RESULT 15
X24976
ID X24976 standard; cDNA; 599 BP.
XX
AC X24976;
XX
DT 05-JUL-1999 (first entry)
XX
DE Mouse TRAIN-R (short form) cDNA.
XX
KW TRAIN-R; receptor; mouse; tumour necrosis factor receptor;
KW agonist; antagonist; cancer; immunological disease; therapy;
KW cytostatic; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 104..556
FT /*tag= a
XX
PN WO9913078-A1.
XX
PD 18-MAR-1999.
XX
PF 11-SEP-1998; 98WO-US19030.
XX
PR 06-MAY-1998; 98US-0084422.
PR 12-SEP-1997; 97US-0058631.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Hession C, Tschopp J;
XX
DR WPI; 1999-229238/19.
DR P-PSDB; W98144.
XX
PT New cysteine-rich tumor necrosis factor receptor
XX
PS Claim 1; Page 26; 30pp; English.
XX
CC The present sequence encodes a novel murine cysteine-rich tumour
CC necrosis factor receptor family member termed TRAIN-R (short form)
CC (see W98144). This putative natural soluble form of murine TRAIN-R
CC may inhibit signalling by the full-length TRAIN-R (see W98145).
CC Murine TRAIN-R is expressed at high levels in brain and lung, and
CC at lower levels in liver, skeletal muscle and kidney. Cell death
CC can be induced by administering an agent capable of inhibiting the
CC binding of TRAIN-R to its ligand. A claimed method of treating, or
CC reducing, the advancement, severity or effects of an immunological
CC disease in a mammal comprises administering a pharmaceutical
CC composition which comprises a TRAIN-R blocking agent, e.g. soluble
CC TRAIN-R. TRAIN-R can be fused to an immunoglobulin molecule to
CC produce a fusion protein which may be targeted to various sites.
CC It can be used in binding assays, and to identify antagonists and
CC agonists. Anti-TRAIN receptor antibodies can be used to reduce the
CC severity of an immune response or to treat cancer. TRAIN-R
CC blocking agents can be used to reduce the severity or effects of an
CC immunological disease (all claimed).
XX
SQ Sequence 599 BP; 149 A; 147 C; 180 G; 123 T; 0 other;

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  Query Match             21.8%;  Score 326.6;  DB 20;  Length 599;
  Best Local Similarity   78.2%;  Pred. No. 4.3e-60;
  Matches  392;  Conservative    0;  Mismatches  109;  Indels    0;  Gaps    0;

Qy      18 caacaataaatacatttgataagaaagatggctttaaaagtgctactagaacaagagaaa 77
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Db      77 caggaataaacacgtttggtgagagccatggcactcaaggtcctacctctacacaggacg 136

Qy      78 acgtttttcactcttttagtattactaggctatttgtcatgtaaagtgacttgtgaaaca 137
             | | ||| ||    |  | || |||  | |  || |||||||||||| ||| |||||
Db     137 gtgctcttcgctgccattctcttcctactccacctggcatgtaaagtgagttgcgaaacc 196

Qy     138 ggagactgtagacagcaagaattcagggatcggtctggaaactgtgttccctgcaaccag 197
           ||||| || || ||||| ||||||| |||||| |||||||||||||| | |||||| |||
Db     197 ggagattgcaggcagcaggaattcaaggatcgatctggaaactgtgtcctctgcaaacag 256

Qy     198 tgtgggccaggcatggagttgtctaaggaatgtggcttcggctatggggaggatgcacag 257
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Db     257 tgcggacctggcatggagttgtccaaggaatgtggcttcggctatggggaggatgcacag 316

Qy     258 tgtgtgacgtgccggctgcacaggttcaaggaggactggggcttccagaaatgcaagccc 317
           |||||| | ||| ||| |||| |||||||||| |||||||| |||||||| || |||||
Db     317 tgtgtgccctgcaggccgcaccggttcaaggaagactggggtttccagaagtgtaagcca 376

Qy     318 tgtctggactgcgcagtggtgaaccgctttcagaaggcaaattgttcagccaccagtgat 377
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Db     377 tgtgcggactgtgcgctggtgaaccgctttcagagggccaactgctcacacaccagtgat 436

Qy     378 gccatctgcggggactgcttgccaggattttataggaagacgaaacttgtcggctttcaa 437
           ||  |||||||||||||| ||||||||||||  ||||||| ||||| || || ||||||
Db     437 gctgtctgcggggactgcctgccaggattttaccggaagaccaaactggttggttttcaa 496

Qy     438 gacatggagtgtgtgccttgtggagaccctcctcctccttacgaaccgcactgtgccagc 497
           |||||||||||||||| || |||||||| |||||||| |||||||| |||||||   |
Db     497 gacatggagtgtgtgccctgcggagacccacctcctccctacgaaccacactgtgagtga 556

Qy     498 aaggtcaacctcgtgaagatc 518
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Db     557 tgtgccaagtggcagcagacc 577


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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 2, 2001, 23:31:01 ; Search time 95.13 Seconds
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Title: US-09-380-276A-7
Perfect score: 1496
Sequence: 1 gggaacgtagaactctccaa.....aaaaaaaaaaaaaaaaaaaa 1496

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Gapop 10.0 , Gapext 1.0

Searched: 280836 seqs, 80580151 residues

Total number of hits satisfying chosen parameters: 561672

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	54.8	3.7	1582	3	US-08-545-196B-10	Sequence 10, Appl
	2	54.8	3.7	1582	3	US-08-545-196B-12	Sequence 12, Appl
c	3	54.4	3.6	3138	1	US-07-867-106-4	Sequence 4, Appli
	4	53	3.5	2007	3	US-08-747-221B-36	Sequence 36, Appl
c	5	53	3.5	2007	3	US-08-747-221B-38	Sequence 38, Appl
	6	52.8	3.5	5173	1	US-08-242-677-1	Sequence 1, Appli
	7	52.6	3.5	1420	2	US-08-909-965C-3	Sequence 3, Appli
	8	52.6	3.5	3238	4	PCT-US94-10080-5	Sequence 5, Appli
	9	52.4	3.5	3581	2	US-08-738-349-1	Sequence 1, Appli
	10	51.8	3.5	3437	3	US-08-860-339-17	Sequence 17, Appl
	11	51.6	3.4	1641	1	US-08-300-903A-8	Sequence 8, Appli
	12	51.2	3.4	991	3	US-08-924-747-25	Sequence 25, Appl
	13	51.2	3.4	1776	3	US-08-655-352-10	Sequence 10, Appl
	14	50.6	3.4	19124	2	US-08-487-826B-13	Sequence 13, Appl
	15	50.2	3.4	3933	1	US-08-199-776-1	Sequence 1, Appli
	16	50.2	3.4	3933	3	US-08-663-731-1	Sequence 1, Appli
	17	50.2	3.4	3933	3	US-08-879-338-1	Sequence 1, Appli
	18	50.2	3.4	3933	4	PCT-US95-02044-1	Sequence 1, Appli
	19	50	3.3	1046	1	US-08-361-467B-4	Sequence 4, Appli
	20	50	3.3	1046	1	US-08-484-332C-4	Sequence 4, Appli
	21	49.8	3.3	8920	2	US-08-446-855A-1	Sequence 1, Appli
	22	49.6	3.3	2700	3	US-09-315-861-1	Sequence 1, Appli
	23	49.2	3.3	2887	4	PCT-US96-10521-14	Sequence 14, Appl
	24	49	3.3	5852	1	US-07-867-106-2	Sequence 2, Appli
	25	48.8	3.3	458	1	US-08-524-757-1	Sequence 1, Appli
c	26	48.6	3.2	1582	3	US-08-545-196B-10	Sequence 10, Appl
c	27	48.6	3.2	1582	3	US-08-545-196B-12	Sequence 12, Appl
	28	48.6	3.2	2589	4	PCT-US96-12860-1	Sequence 1, Appli
	29	48.4	3.2	1393	1	US-08-174-467-18	Sequence 18, Appl
	30	48.4	3.2	1393	3	US-08-452-071-18	Sequence 18, Appl
	31	48.4	3.2	1490	2	US-08-553-367A-5	Sequence 5, Appli
	32	48.2	3.2	1952	1	US-08-333-358-1	Sequence 1, Appli
	33	48.2	3.2	1952	1	US-08-463-694-1	Sequence 1, Appli
	34	48.2	3.2	1952	1	US-08-694-501-1	Sequence 1, Appli
	35	48.2	3.2	2619	4	PCT-US96-10521-17	Sequence 17, Appl
c	36	48	3.2	2760	1	US-08-101-593-3	Sequence 3, Appli
	37	47.6	3.2	3207	1	US-07-946-497-1	Sequence 1, Appli
	38	47.6	3.2	3207	1	US-08-483-322-1	Sequence 1, Appli
	39	47.6	3.2	3207	2	US-08-478-882-1	Sequence 1, Appli
	40	47.4	3.2	10136	1	US-08-353-700-2	Sequence 2, Appli
	41	47.4	3.2	10136	4	PCT-US95-16216-2	Sequence 2, Appli
	42	47.2	3.2	1804	2	US-08-504-459-5	Sequence 5, Appli
	43	46.8	3.1	748	1	US-08-361-467B-3	Sequence 3, Appli
	44	46.8	3.1	748	1	US-08-484-332C-3	Sequence 3, Appli
	45	46.8	3.1	1098	3	US-09-248-335-35	Sequence 35, Appl

ALIGNMENTS

```
RESULT   1
US-08-545-196B-10
; Sequence 10, Application US/08545196B
; Patent No. 6080577
;  GENERAL INFORMATION:
;    APPLICANT:  MELKI, JUDITH
;    APPLICANT:  MUNNICH, ARNOLD
;    TITLE OF INVENTION:  SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
;    TITLE OF INVENTION:  FOR SPINAL MUSCULAR ATROPHY
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIRCH, STEWART, KOLASCH AND BIRCH, LLP
;      STREET:  PO BOX 747
;      CITY:  FALLS CHURCH
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22040-0747
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/545,196B
;      FILING DATE:  19-OCT-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FARACI, C. J.
;      REGISTRATION NUMBER:  32,350
;      REFERENCE/DOCKET NUMBER:  2121-110P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 205-8000
;      TELEFAX:  (703) 205-8050
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1582 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-545-196B-10


  Query Match             3.7%;  Score 54.8;  DB 3;  Length 1582;
  Best Local Similarity   67.5%;  Pred. No. 0.00016;
  Matches   77;  Conservative    0;  Mismatches   37;  Indels    0;  Gaps    0;

Qy   1383 gttttttttttgcatctttaataatttcttgtatgttgtagagtatgttttaaaataaat 1442
           | | ||  ||    | |||  |  | |||| ||| |  |  |   | | | | || ||
Db   1417 GCTGTTCATTGTACTGTTTTTTTCTATCTTCTATATGTTTAAAAGTATATAATAAAAATA 1476
```

```
Qy   1443 ttcaagtatttttttttaaaaactaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 1496
          || || | ||||||  |||||  ||||||||||||||||||||||||||||||
Db   1477 TTTAATTTTTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1530


RESULT   2
US-08-545-196B-12
; Sequence 12, Application US/08545196B
; Patent No. 6080577
;  GENERAL INFORMATION:
;    APPLICANT:  MELKI, JUDITH
;    APPLICANT:  MUNNICH, ARNOLD
;    TITLE OF INVENTION:  SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
;    TITLE OF INVENTION:  FOR SPINAL MUSCULAR ATROPHY
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIRCH, STEWART, KOLASCH AND BIRCH, LLP
;      STREET:  PO BOX 747
;      CITY:  FALLS CHURCH
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22040-0747
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/545,196B
;      FILING DATE:  19-OCT-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FARACI, C. J.
;      REGISTRATION NUMBER:  32,350
;      REFERENCE/DOCKET NUMBER:  2121-110P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 205-8000
;      TELEFAX:  (703) 205-8050
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1582 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-545-196B-12


  Query Match             3.7%;  Score 54.8;  DB 3;  Length 1582;
  Best Local Similarity   67.5%;  Pred. No. 0.00016;
  Matches   77;  Conservative    0;  Mismatches   37;  Indels    0;  Gaps    0;

Qy   1383 gttttttttttgcatctttaataatttcttgtatgttgtagagtatgttttaaaataaat 1442
          | | ||  ||    | |||  |  | |||| ||| |  |  |   | | | | || ||
Db   1417 GCTGTTCATTGTACTGTTTTTTTCTATCTTCTATATGTTTAAAAGTATATAATAAAAATA 1476

Qy   1443 ttcaagtatttttttttaaaaactaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 1496
          || || | ||||||  |||||  ||||||||||||||||||||||||||||||
Db   1477 TTTAATTTTTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1530


RESULT   3
US-07-867-106-4/c
; Sequence 4, Application US/07867106
; Patent No. 5389526
;  GENERAL INFORMATION:
;    APPLICANT:  Slade, Martin B
;    APPLICANT:  Chang, Andy C M
;    APPLICANT:  Williams, Keith L
;    TITLE OF INVENTION:  Improved Plasmid Vectors for Cellular
;    TITLE OF INVENTION:  Slime Moulds of the Genus Dictyostelium
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
;      STREET:  One Liberty Place 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/867,106
;      FILING DATE:  19920625
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  AU PJ 7187
;      APPLICATION NUMBER:  PCT/AU90/00530
;      FILING DATE:  02-NOV-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Feeney, Joanne Longo
;      REGISTRATION NUMBER:  35,134
;      REFERENCE/DOCKET NUMBER:  RICE-0002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-568-3100
;      TELEFAX:  215-568-3439
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3138 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  DNA (genomic)
;    ANTI-SENSE:  NO
US-07-867-106-4


  Query Match             3.6%;  Score 54.4;  DB 1;  Length 3138;
  Best Local Similarity   62.5%;  Pred. No. 0.00028;
  Matches   85;  Conservative    0;  Mismatches   51;  Indels    0;  Gaps    0;

Qy   1361 aagatttgggggaacctgatgagtttttttttgcatctttaataatttcttgtatgttg 1420
          ||  | ||  |||| | ||   | |||||| |  |  || | | |||| || || |
Db   2087 AATGTATGTTGGAATTTCATTTTTATTTTTTATTTAATTTAATTTATTTGTTTTAAGAAA 2028

Qy   1421 tagagtatgttttaaaataaatttcaagtatttttttttaaaaactaaaaaaaaaaaaaaa 1480
          ||    |      |||| ||| |    |||    | | |||| ||||||||||||||||
Db   2027 TAAGAAAAAAAAAAAAAAAAAAATCTTTTTATGCAATCTGAAAAAAAAAAAAAAAAAAAAA 1968

Qy   1481 aaaaaaaaaaaaaaaa 1496
          ||||||||||||||||
Db   1967 AAAAAAAAAAAAAAAA 1952


RESULT   4
US-08-747-221B-36
; Sequence 36, Application US/08747221B
; Patent No. 6063610
;  GENERAL INFORMATION:
;    APPLICANT:  Silver, Gary W.
;    APPLICANT:  Wisnewski, Nancy
;    TITLE OF INVENTION:  No. 6063610el Carboxylesterase Nucleic Acid
;    TITLE OF INVENTION:  Molecules, Proteins and Uses Thereof
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carol Talkington Verser, Ph.D.
;      ADDRESSEE:  Heska Corporation
;      STREET:  1825 Sharp Point Drive
;      CITY:  Fort Collins
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80525
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  Windows 95
;       SOFTWARE:  WordPerfect for Windows, Version 7.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/747,221B
;       FILING DATE:  No. 6063610ember 12, 1996
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Verser, Carol Talkington
;       REGISTRATION NUMBER:  37,459
;       REFERENCE/DOCKET NUMBER:  FC-1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  970/493-7272
;       TELEFAX:  970/484-9505
;   INFORMATION FOR SEQ ID NO:  36:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2007 nucleotides
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  11..1594
US-08-747-221B-36


  Query Match             3.5%;  Score 53;  DB 3;  Length 2007;
  Best Local Similarity   67.9%;  Pred. No. 0.0005;
  Matches   74;  Conservative    0;  Mismatches   35;  Indels    0;  Gaps    0;

Qy   1384 ttttttttttgcatctttaataatttcttgtatgttgtagagtatgttttaaaataaatt 1443
           || ||    |   | | | ||| || ||| ||| || |    | | |||||    ||||
Db   1899 TTATTACCATCTTTGTATCATATTTGCTTTTATTTTTTCATTTTTTTTTTTATTTCAAATA 1958

Qy   1444 tcaagtatttttttttaaaaactaaaaaaaaaaaaaaaaaaaaaaaaaaa 1492
           |   || ||||| | |||||  ||||||||||||||||||||||||||
Db   1959 TATTGTTTTTTTTATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2007


RESULT   5
US-08-747-221B-38/c
; Sequence 38, Application US/08747221B
; Patent No. 6063610
; GENERAL INFORMATION:
;     APPLICANT:  Silver, Gary W.
;     APPLICANT:  Wisnewski, Nancy
;     TITLE OF INVENTION:  No. 6063610el Carboxylesterase Nucleic Acid
;     TITLE OF INVENTION:  Molecules, Proteins and Uses Thereof
;     NUMBER OF SEQUENCES:  66
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Carol Talkington Verser, Ph.D.
;       ADDRESSEE:  Heska Corporation
;       STREET:  1825 Sharp Point Drive
;       CITY:  Fort Collins
;       STATE:  Colorado
;       COUNTRY:  USA
;       ZIP:  80525
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  Windows 95
;       SOFTWARE:  WordPerfect for Windows, Version 7.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/747,221B
;       FILING DATE:  No. 6063610ember 12, 1996
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Verser, Carol Talkington
;       REGISTRATION NUMBER:  37,459
;       REFERENCE/DOCKET NUMBER:  FC-1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  970/493-7272
;       TELEFAX:  970/484-9505
;   INFORMATION FOR SEQ ID NO:  38:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2007 nucleotides
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-08-747-221B-38


  Query Match             3.5%;  Score 53;  DB 3;  Length 2007;
  Best Local Similarity   67.9%;  Pred. No. 0.0005;
  Matches   74;  Conservative    0;  Mismatches   35;  Indels    0;  Gaps    0;

Qy   1384 ttttttttttgcatctttaataatttcttgtatgttgtagagtatgttttaaaataaatt 1443
           || ||    |   | | | ||| || ||| ||| || |    | | |||||    ||||
Db    109 TTATTACCATCTTTGTATCATATTTGCTTTTATTTTTTCATTTTTTTTTTTATTTCAAATA 50

Qy   1444 tcaagtatttttttttaaaaactaaaaaaaaaaaaaaaaaaaaaaaaaaa 1492
           |   || ||||| | |||||  ||||||||||||||||||||||||||
Db     49 TATTGTTTTTTTTATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT   6
US-08-242-677-1
; Sequence 1, Application US/08242677
; Patent No. 5677143
; GENERAL INFORMATION:
;     APPLICANT:  Gaynor, Richard B
;     APPLICANT:  Wu, Foon W.
;     TITLE OF INVENTION:  Cellular Nucleic Acid Binding Protein
;     TITLE OF INVENTION:  and Uses Thereof in regulating Gene Expression and in the
;     TITLE OF INVENTION:  Treatment of AIDS
;     NUMBER OF SEQUENCES:  9
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Arnold, White & Durkee
;       STREET:  P.O. Box 4433
;       CITY:  Houston
;       STATE:  TX
;       COUNTRY:  USA
;       ZIP:  77210
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/242,677
;       FILING DATE:
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Mayfield, Denise L.
;       REGISTRATION NUMBER:  33,732
;       REFERENCE/DOCKET NUMBER:  UTSD:401
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  713-787-1400
;       TELEFAX:  713-789-2679
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  5173 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..4863
US-08-242-677-1


  Query Match             3.5%;  Score 52.8;  DB 1;  Length 5173;
  Best Local Similarity   67.0%;  Pred. No. 0.00086;
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```
  Matches   75;  Conservative    0;  Mismatches   37;  Indels    0;  Gaps    0;

Qy   1385 ttttttttgcatctttaataatttcttgtatgttgtagagtatgttttaaaataaattt 1444
          | ||||      |  | || | ||| |  ||  |||||   |   ||| | || | ||||
Db   5028 TATTTTCCCCTTTAATAAACACTTTTTGTTAAATTGTATTCTTCCTTTAATAAAATATTT 5087

Qy   1445 caagtatttttttttaaaaactaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 1496
           ||| | || |   | |||  ||||||||||||||||||||||||||||||||
Db   5088 TAAGCAATTGTCCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5139


RESULT   7
US-08-909-965C-3
; Sequence 3, Application US/08909965C
; Patent No. 5936078
;  GENERAL INFORMATION:
;    APPLICANT:  Kuga Tetsro
;    APPLICANT:  Nakagawa Satoshi
;    APPLICANT:  Sakaki yoshiyuki
;    APPLICANT:  Zhao Nanding
;    APPLICANT:  Hashida Hideji
;    TITLE OF INVENTION:  NOVEL DNA, NOVEL POLYPEPTIDE
;    TITLE OF INVENTION:  AND NOVEL ANTIBODY
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FITZPATRICK, CELLA, HARPER AND SCINTO
;      STREET:  277 Park Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10172-0194
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/909,965C
;      FILING DATE:  August 12, 1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 322745/95
;      APPLICATION NUMBER:  PCT/JP96/03630
;      FILING DATE:  12-No. 5936078-1995
;      FILING DATE:  12-Dec-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lawrence S. Perry
;      REGISTRATION NUMBER:  31865
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-2400
;      TELEFAX:  212-758-2982
;      TELEX:  236262
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1420 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  human
;    IMMEDIATE SOURCE:
;      CLONE:  F198
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  378 to 575
;      LOCATION:  590 to 709
;      LOCATION:  1105 to 1206
;      IDENTIFICATION METHOD:  by experiment
US-08-909-965C-3


Query Match             3.5%;  Score 52.6;  DB 2;  Length 1420;
  Best Local Similarity   66.1%;  Pred. No. 0.00054;
  Matches   76;  Conservative    0;  Mismatches   39;  Indels    0;  Gaps    0;

Qy   1382 agttttttttttgcatctttaataatttcttgtatgttgtagagtatgttttaaaataaa 1441
          ||| ||||  |||  |||||   | |||||     |  |    |      | |  ||| |||
Db   1302 AGTATTTTGGTTGGCTCTTTGTGATTTTCTACACAGAAGATTATGTCATCTACAAACAAA 1361

Qy   1442 tttcaagtatttttttttaaaaactaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 1496
          | | |   |   || || |||||  ||||||||||||||||||||||||||||||
Db   1362 TATAATTTTACTTCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1416


RESULT   8
PCT-US94-10080-5
; Sequence 5, Application PC/TUS9410080
;  GENERAL INFORMATION:
;    APPLICANT:  GENETICS INSTITUTE, INC.
;    TITLE OF INVENTION:  RECEPTOR PROTEINS
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute Inc.- Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10080
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/123,934
;      FILING DATE:  17-SEP-1993
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  LAZAR, Steven R
;      REGISTRATION NUMBER:  32,618
;      REFERENCE/DOCKET NUMBER:  5203-PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 498-8260
;      TELEFAX:  (617) 876-5851
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3238 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    IMMEDIATE SOURCE:
;      CLONE:  CFK1-10a
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  474..2000
PCT-US94-10080-5


  Query Match             3.5%;  Score 52.6;  DB 4;  Length 3238;
  Best Local Similarity   68.2%;  Pred. No. 0.00078;
  Matches   73;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy   1390 ttttgcatctttaataatttcttgtatgttgtagagtatgttttaaaataaatttcaagt 1449
          | ||   | || |   | || |||||| | ||||    |  | |||| |||||      ||
Db   3091 TATTTTGTTTTAATCTACTTTTTGTATTTAGTAGTTATTTGTATAAATTAAATAAACTGT 3150

Qy   1450 attttttttaaaaactaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 1496
           ||    | |||||  ||||||||||||||||||||||||||||||
Db   3151 TTTCAAGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3197
```

```
RESULT   9
US-08-738-349-1
; Sequence 1, Application US/08738349
; Patent No. 5869638
;  GENERAL INFORMATION:
;    APPLICANT:  Takeshita, Sunao
;    APPLICANT:  Okazaki, Makoto
;    APPLICANT:  Kawai, Shinji
;    APPLICANT:  Tsujimura, Atsushi
;    APPLICANT:  Amann, Egon
;    TITLE OF INVENTION:  Bone-Related Cadherin-Like Protein and
;    TITLE OF INVENTION:  Process for Its Production
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/738,349
;      FILING DATE:  25-OCT-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/364,439
;      FILING DATE:
;      APPLICATION NUMBER:  US 08/112,061
;      FILING DATE:  26-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Barker, M. P.
;      REGISTRATION NUMBER:  32,013
;      REFERENCE/DOCKET NUMBER:  02481.1323-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-408-4000
;      TELEFAX:  202-408-4400
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3581 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Mus musculus
;      STRAIN:  osteoblastic cell line MC3T3E1
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  284..2671
US-08-738-349-1


  Query Match             3.5%;  Score 52.4;  DB 2;  Length 3581;
  Best Local Similarity   67.3%;  Pred. No. 0.00091;
  Matches   74;  Conservative    0;  Mismatches   36;  Indels    0;  Gaps    0;

Qy   1387 ttttttgcatctttaataatttcttgtatgttgtagagtatgttttaaaataaatttca 1446
           || |  ||   ||||||||    |||  || | . |    |  ||| |||  |||
Db   3434 TTGTACTGTTGCTTTAATATGAGCTTCAATATAAGAAGCAACCTTTGAAATAAAAAAAG 3493

Qy   1447 agtatttttttttaaaaactaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 1496
          | | ||||||  |||||  ||||||||||||||||||||||||||||||||
Db   3494 ATTCTTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3543


RESULT  10
US-08-860-339-17
; Sequence 17, Application US/08860339
; Patent No. 6117665
; GENERAL INFORMATION:
;  APPLICANT: Kossmann, Jens
;  APPLICANT: Emmermann, Michael
;  APPLICANT: Virgin, Ivar
;  APPLICANT: Renz, Andreas
;  TITLE OF INVENTION: DNA MOLECULES CODING FOR DEBRANCHING ENZYMES DERIVED
;  TITLE OF INVENTION: FROM PLANTS
;  FILE REFERENCE: AGREVO-6
;  CURRENT APPLICATION NUMBER: US/08/860,339
;  CURRENT FILING DATE: 1997-11-25
;  EARLIER APPLICATION NUMBER: DE P4447387.7
;  EARLIER FILING DATE: 1994-12-22
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
;   LENGTH: 3437
;   TYPE: DNA
;   ORGANISM: Spinacia oleracea
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (201)..(3095)
US-08-860-339-17


  Query Match             3.5%;  Score 51.8;  DB 3;  Length 3437;
  Best Local Similarity   60.1%;  Pred. No. 0.0013;
  Matches   86;  Conservative    0;  Mismatches   57;  Indels    0;  Gaps    0;

Qy   1354 ccagcataagatttgggggaacctgatgagtttttttttgcatctttaataatttcttg 1413
           ||| || ||  ||  |  | || ||  |   |  |||| |    | | ||||||   |||
Db   3288 ccaccaaaatcttacgttgtacttgtagcagtgcttttgtcacgcataaataatcagttg 3347

Qy   1414 tatgttgtagagtatgttttaaaataaatttcaagtatttttttttaaaaactaaaaaaaa 1473
            ||||   |          |   |    | |  | ||||||||  ||||  ||||||||
Db   3348 cttgttaaccatacatccgatatgaatgaataatttttttttttttttaaaaaaaaaaaaa 3407

Qy   1474 aaaaaaaaaaaaaaaaaaaaaa 1496
          ||||||||||||||||||||||
Db   3408 aaaaaaaaaaaaaaaaaaaaaa 3430


RESULT  11
US-08-300-903A-8
; Sequence 8, Application US/08300903A
; Patent No. 5591630
;  GENERAL INFORMATION:
;    APPLICANT:  Anderson, Dirk M
;    APPLICANT:  Giri, Judith G
;    TITLE OF INVENTION:  Interleukin-15 Receptors
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Apple Operating System 7.1
;      SOFTWARE:  Microsoft Word for Apple, Version 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/300,903A
;      FILING DATE:  06-SEPTEMBER-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/236,919
;      FILING DATE:  06-MAY-1994
;      CLASSIFICATION:  435
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Perkins, Patricia Anne
;      REGISTRATION NUMBER:  34,695
;      REFERENCE/DOCKET NUMBER:  2822-A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  206-587-0430
;      TELEFAX:  206-233-0644
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1641 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  3..839
US-08-300-903A-8


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  Best Local Similarity   63.9%;  Pred. No. 0.001;
  Matches   78;  Conservative    0;  Mismatches   44;  Indels    0;  Gaps    0;

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          |||   |   || | | | | |||  |  || |||| |  | ||   | |    |  | ||
Db   1467 CCTTGTCTATTATATCTATACATTATATATTATTTGTATTTTGACATTGTACCTTGTATA 1526

Qy   1435 aaataaatttcaagtatttttttttaaaaactaaaaaaaaaaaaaaaaaaaaaaaaaaaa 1494
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Db   1527 AACAAAATAAAACATCTATTTTCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1586

Qy   1495 aa 1496
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Db   1587 AA 1588


RESULT  12
US-08-924-747-25
; Sequence 25, Application US/08924747
; Patent No. 6063570
;  GENERAL INFORMATION:
;    APPLICANT:  MCGONIGLE, BRIAN
;    APPLICANT:  O'KEEFE, DANIEL
;    TITLE OF INVENTION:  SOYBEAN GLUTATHIONE-S-TRANSFERASE
;    TITLE OF INVENTION:  ENZYMES
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  E.I. DU PONT DE NEMOURS AND COMPANY
;      STREET:  1007 MARKET STREET
;      CITY:  WILMINGTON
;      STATE:  DELAWARE
;      COUNTRY:  UNITED STATES OF AMERICA
;      ZIP:  19898
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  DISKETTE, 3.50 INCH
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  MICROSOFT WORD FOR WINDOWS 95
;      SOFTWARE:  MICROSOFT WORD VERSION 7.0A
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/924,747
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FLOYD, LINDA AXAMETHY
;      REGISTRATION NUMBER:  33,692
;      REFERENCE/DOCKET NUMBER:  CL-1108
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  302-892-8112
;      TELEFAX:  302-773-0164
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  991 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      TISSUE TYPE:  SOYBEAN
;    IMMEDIATE SOURCE:
;      CLONE:  SSM.PK0067.G5
US-08-924-747-25


  Query Match             3.4%;  Score 51.2;  DB 3;  Length 991;
  Best Local Similarity   64.2%;  Pred. No. 0.001;
  Matches   77;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;

Qy   1377 tgatgagttttttttttgcatctttaataatttcttgtatgttgtagagtatgtttaaa 1436
          || |  |||||   |||   |   |  | ||  |||  | |||   | | |  ||| ||
Db    846 TGTTCTGTTTTAAATTTAATTGACTGTGATTTGGTTGGGTATTGGCTATTTTAATTTTAA 905

Qy   1437 ataaatttcaagtatttttttttaaaaactaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 1496
           ||||      ||    |||| |||||  ||||||||||||||||||||||||||||||
Db    906 CTAAAAAAAGTGTTCAGTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 965


RESULT  13
US-08-655-352-10
; Sequence 10, Application US/08655352
; Patent No. 6077991
;  GENERAL INFORMATION:
;    APPLICANT:  Bachettira W. Poovaiah, Zhihua Liu,
;    APPLICANT:  Shameekumar Patil, Daisuke Takezawa
;    TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR
;    TITLE OF INVENTION:  PRODUCTION OF MALE-STERILE PLANTS
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klarquist Sparkman Campbell Leigh &
;      ADDRESSEE:  Whinston, LLP
;      STREET:  One World Trade Center
;      STREET:  121 S.W. Salmon Street
;      STREET:  Suite 1600
;      CITY:  Portland
;      STATE:  Oregon
;      COUNTRY:  United States of America
;      ZIP:  97204
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Disk, 3-1/2 inch
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  MS DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/655,352
;      FILING DATE:
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/323,449
;      FILING DATE:  October 14, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dow, Alan. E.
;      REGISTRATION NUMBER:  35,123
;      REFERENCE/DOCKET NUMBER:  4630-45000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (503) 226-7391
;      TELEFAX:  (503) 228-9446
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1776 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double stranded
;      TOPOLOGY:  linear
```

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;    MOLECULE TYPE:  cDNA to mRNA
;      DESCRIPTION:  Tobacco CCaMK cDNA and deduced amino-acid
;      DESCRIPTION:  sequence
;    FEATURE:
;      NAME/KEY:  protein-coding sequence (not including
;      NAME/KEY:  stop codon)
;      LOCATION:  nucleotides 20-1570
US-08-655-352-10


  Query Match             3.4%;  Score 51.2;  DB 3;  Length 1776;
  Best Local Similarity   68.3%;  Pred. No. 0.0013;
  Matches   71;  Conservative    0;  Mismatches   33;  Indels    0;  Gaps    0;

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Qy   1453 ttttttaaaaactaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 1496
          | |  ||||||  ||||||||||||||||||||||||||||||
Db   1716 TATGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1759


RESULT  14
US-08-487-826B-13
; Sequence 13, Application US/08487826B
; Patent No. 5993827
;  GENERAL INFORMATION:
;    APPLICANT:  Sim, Kim L.
;    APPLICANT:  Chitnis, Chetan
;    APPLICANT:  Miller, Louis H.
;    APPLICANT:  Peterson, David S.
;    APPLICANT:  Su, Xin-zhaun
;    APPLICANT:  Wellems, Thomas E.
;    TITLE OF INVENTION:  BINDING DOMAINS FROM PLASMODIUM VIVAX
;    TITLE OF INVENTION:  AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe Martens Olson & Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/487,826B
;      FILING DATE:  10-SEP-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Israelsen, Ned
;      REGISTRATION NUMBER:  29,655
;      REFERENCE/DOCKET NUMBER:  NIH121.001CP1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 235-8550
;      TELEFAX:  (619) 235-0176
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19124 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-487-826B-13


  Query Match             3.4%;  Score 50.6;  DB 2;  Length 19124;
  Best Local Similarity   63.6%;  Pred. No. 0.0054;
  Matches   77;  Conservative    0;  Mismatches   44;  Indels    0;  Gaps    0;

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Db  18238 AACTAATTTCTTATTTTTATTTAACTTTATTCCTTTTTAATTTCTTAATTCTTTTATCAA 18297

Qy   1434 aaaataaatttcaagtatttttttttaaaaactaaaaaaaaaaaaaaaaaaaaaaaaaa 1493
          | || |||  | ||||| || |    |  |  ||||||||||||||||||||||||||
Db  18298 ACAAAAAACATAAAGTAATTCTACATATCAACAAAAAAAAAAAAAAAAAAAAAAAAAA 18357

Qy   1494 a 1494
          |
Db  18358 A 18358


RESULT  15
US-08-199-776-1
; Sequence 1, Application US/08199776
; Patent No. 5594120
;  GENERAL INFORMATION:
;    APPLICANT:  Brenner, Michael B.
;    APPLICANT:  Parker, Christina M.
;    TITLE OF INVENTION:  No. 5594120el integrin alpha subunit
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield and Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/199,776
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plumer, Elizabeth R.
;      REGISTRATION NUMBER:  36,637
;      REFERENCE/DOCKET NUMBER:  B0801/7020
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3933 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  mucosal lymphocyte
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  126..3662
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  180..3659
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  126..179
US-08-199-776-1


  Query Match             3.4%;  Score 50.2;  DB 1;  Length 3933;
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Best Local Similarity 81.7%; Pred. No. 0.0033;
Matches 58; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Db   3848 TTTGGTATTAAATAAATTTACACTTTTCTTTGCAAAAAAAAAAAAAAAAAAAAAAAAAAA 3907

Qy   1486 aaaaaaaaaaa 1496
          ||||||||||
Db   3908 AAAAAAAAAAA 3918
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Search completed: March 3, 2001, 04:40:32
Job time: 18571 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 2, 2001, 20:24:05 ; Search time 889.38 Seconds
(without alignments)
11787.089 Million cell updates/sec

Title: US-09-380-276A-7
Perfect score: 1496
Sequence: 1 gggaacgtagaactctccaa.....aaaaaaaaaaaaaaaaaaa 1496

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7991742 seqs, 3503743858 residues

Total number of hits satisfying chosen parameters: 15983484

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
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2: gb_est2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		425.2	28.4	454	147	W56629	W56629 zd16e11.r1
2		302.2	20.2	395	106	BE306459	BE306459 601103459
3		274.8	18.4	282	28	AL036000	AL036000 DKFZp564K
4		264.8	17.7	534	135	BE757704	BE757704 212225 MA
5		215.6	14.4	401	1	AA003356	AA003356 mg49g01.r
6		192.8	12.9	369	91	AW478317	AW478317 19558 MAR
7		186.6	12.5	358	1	AA036247	AA036247 mi74a03.r
8		157.6	10.5	258	133	BB542020	BB542020 BB542020
9		155	10.4	643	159	AQ563354	AQ563354 HS_5335_B
10		125.8	8.4	646	159	AQ544065	AQ544065 RPCI-11-3
11		124.4	8.3	275	31	AV111112	AV111112 AV111112
12		120.8	8.1	404	8	AA495217	AA495217 fa04d10.r
13	c	113.8	7.6	450	158	AQ514075	AQ514075 HS_5184_A
14		95	6.4	1110	193	CNS05OTC	AL347097 Tetraodon
15	c	91.2	6.1	414	91	AW527025	AW527025 UI-R-BO1-
16		80.2	5.4	381	21	AI551729	AI551729 vf11e02.y
17		67.4	4.5	442	109	BE554624	BE554624 ur48c11.y
18	c	63	4.2	996	138	BE966927	BE966927 601660947
19		62	4.1	240	29	AU074171	AU074171 AU074171
20	c	61.8	4.1	240	29	AU074171	AU074171 AU074171
21		61.6	4.1	734	191	CNS024WE	AL181319 Tetraodon
22		61.2	4.1	207	29	AU037991	AU037991 AU037991
23	c	61	4.1	495	10	AA676361	AA676361 ad38a04.s
24		61	4.1	746	191	CNS033OX	AL226410 Tetraodon
25		60.8	4.1	357	140	C91149	C91149 C91149 Dict
26		60.8	4.1	591	87	AW187044	AW187044 BNLGH1918
27	c	60.4	4.0	710	106	BE317688	BE317688 NF053F10L
28		60.2	4.0	434	111	BE722937	BE722937 192212 MA
29		59.8	4.0	153	190	CNS015IE	AL105488 Drosophil
30		59.8	4.0	786	190	CNS009A5	AL053317 Drosophil
31	c	59.8	4.0	928	190	CNS00DKY	AL071865 Drosophil
32		59.6	4.0	583	192	CNS044QG	AL274417 Tetraodon
33		59.2	4.0	231	3	AA185470	AA185470 mu47f06.r
34		59.2	4.0	497	29	AU038067	AU038067 AU038067
35		59.2	4.0	625	191	CNS036A2	AL229763 Tetraodon
36		59.2	4.0	690	140	C93837	C93837 C93837 Dict
37		59.2	4.0	996	138	BE966927	BE966927 601660947
38	c	59.2	4.0	1101	190	CNS00Z38	AL097166 Drosophil
39	c	59	3.9	405	150	AQ173919	AQ173919 HS_3204_A
40		59	3.9	495	93	AW644074	AW644074 cm37b04.w
41	c	58.8	3.9	586	191	CNS02B9C	AL189561 Tetraodon
42		58.4	3.9	330	29	AU037574	AU037574 AU037574
43	c	58.4	3.9	362	23	AI673278	AI673278 tw69e12.x
44	c	58.4	3.9	637	191	CNS036CC	AL229845 Tetraodon
45		58.4	3.9	867	190	CNS00CX5	AL060052 Drosophil

ALIGNMENTS

RESULT 1
W56629
LOCUS W56629 454 bp mRNA EST 15-OCT-1996
DEFINITION zd16e11.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:340844 5', mRNA sequence.
ACCESSION W56629
VERSION W56629.1 GI:1358487
KEYWORDS EST.
SOURCE human.

```
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 454)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
            ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
            Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
            ,R., Williamson,A., Wohldmann,P. and Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1373   Std Error: 0.00
            Seq primer: mob.REGA+ET.
FEATURES             Location/Qualifiers
     source          1. .454
                     /organism="Homo sapiens"
                     /db_xref="GDB:1266219"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:340844"
                     /clone_lib="Soares_fetal_heart_NbHH19W"
                     /sex="unknown"
                     /dev_stage="19 weeks"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATCTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by
                     M.Fatima Bonaldo. This library was constructed from the
                     same fetus as the fetal lung library, Soares fetal lung
                     NbHL19W."
BASE COUNT      132 a     96 c     88 g    138 t
ORIGIN


  Query Match             28.4%;  Score 425.2;  DB 147;  Length 454;
  Best Local Similarity   97.8%;  Pred. No. 1.5e-85;
  Matches  442;  Conservative    0;  Mismatches    8;  Indels    2;  Gaps    1;

Qy   1016 ctcttatcctgaactcactggagaagacattcattctctcaatccagaacttgaaagctc 1075
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CTCTTATCCTGAACTCACTGGAGAAGACATTCATTCTCTCAATCCAGAACTTGAAAGCTC 60

Qy   1076 aacgtctttggattcaaatagcagtcaagatttggttggtggggctgttccagtccagtc 1135
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AACGTCTTTGGATTCAAATAGCAGTCAAGATTTGGTTGGTGGGGCTGTTCCAGTCCAGTC 120

Qy   1136 tcattctgaaaactttacagcagctactgatttatctagatataacaacacactggtaga 1195
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TCATTCTGAAAACTTTACAGCAGCTACTGATTTATCTAGATATAACAACACACTGGTAGA 180

Qy   1196 atcagcatcaactcaggatgcactaactatgagaagccagctagatcaggagagtggcgc 1255
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ATCAGCATCAACTCAGGATGCACTAACTATGAGAAGCCAGCTAGATCAGGAGAGTGGCGC 240

Qy   1256 tatcatccacccagccactcagacgtccctccaggtaaggcagcgactgggttccctgtg 1315
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TGTCATCCACCCAGCCACTCAGACGTCCCTCCAGGTAAGGCAGCGACTGGGTTCCCTGTG 300

Qy   1316 aacacagcactgacttacagtagatcagaactctgttcccagcataagatttgggggaac 1375
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AACACAGCACTGACTTACAGTAGATCAGAACTCTGTTCCCAGCATAAGATTTGGGGGAAC 360

Qy   1376 ctg--atgagtttttttttttgcatctttaataatttcttgtatgttgtagagtatgtttt 1433
           |||      ||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db    361 CTGGATGAGTTTTTTTTTTTGCATCTTTAATAATTTCTTATATGTTGTAGAGTATGTTTT 420

Qy   1434 aaaataaatttcaagtatttttttttaaaaact 1465
           ||||||||||||||||||||||| |||||||
Db    421 AAAATAAATTTCAAGTATTTTTTTAAAAAACT 452


RESULT   2
BE306459
LOCUS       BE306459      395 bp    mRNA            EST       13-JUL-2000
DEFINITION  601103459F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3495566 5',
            mRNA sequence.
ACCESSION   BE306459
VERSION     BE306459.1  GI:9159707
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 395)
  AUTHORS   NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM8546  row: f  column: 15
            High quality sequence stop: 395.
FEATURES             Location/Qualifiers
     source          1. .395
                     /organism="Mus musculus"
                     /strain="CZECH II (feral)"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:3495566"
                     /clone_lib="NCI_CGAP_Lu29"
                     /tissue_type="spontaneous tumor, metastatic to mammary.
                     Stem cell origin."
                     /lab_host="DH10B"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigator
                     providing samples: Gilbert Smith, NIH"
BASE COUNT       88 a    101 c    120 g     86 t
ORIGIN


  Query Match             20.2%;  Score 302.2;  DB 106;  Length 395;
  Best Local Similarity   85.3%;  Pred. No. 7e-58;
  Matches  337;  Conservative    0;  Mismatches   58;  Indels    0;  Gaps    0;

Qy    100 tactaggctatttgtcatgtaaagtgacttgtgaaacaggagactgtagacagcaagaat 159
          | |||  | | ||| |||||||||||| ||| ||||| ||||| || || ||||| ||||
Db      1 TCCTACTCCACTTGGCATGTAAAGTGAGTTGCGAAACCGGAGATTGCAGGCAGCAGGAAT 60

Qy    160 tcagggatcggtctggaaactgtgttccctgcaaccagtgtgggccaggcatggagttgt 219
          ||| |||||| |||||||||||||| | |||||| ||||| || || ||||||||||||||
Db     61 TCAAGGATCGATCTGGAAACTGTGTCCTCTGCAAACAGTGCGGACCTGGCATGGAGTTGT 120

Qy    220 ctaaggaatgtggcttcggctatggggaggatgcacagtgtgtgacgtgccggctgcaca 279
          | |||||||||||||||||||||||||||||||||||||||||| | ||| ||| ||||
Db    121 CCAAGGAATGTGGCTTCGGCTATGGGGAGGATGCACAGTGTGTGCCCTGCAGGCCGCACC 180

Qy    280 ggttcaaggaggactggggcttccagaaatgcaagccctgtctggactgcgcagtggtga 339
```

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          |||||||||| |||||||| |||||||| || ||||| ||| ||||||| ||  |||||||
Db    181 GGTTCAAGGAAGACTGGGGTTTCCAGAAGTGTAAGCCGTGTGCGGACTGTGCGCTGGTGA 240

Qy    340 accgctttcagaaggcaaattgttcagccaccagtgatgccatctgcggggactgcttgc 399
          |||||||||||| ||| || || ||| |||||||||||  |||||||||||||| |||
Db    241 ACCGCTTTCAGAGGGCCAACTGCTCACACACCAGTGATGCTGTCTGCGGGGACTGCCTGC 300

Qy    400 caggattttataggaagacgaaacttgtcggctttcaagacatggagtgtgtgccttgtg 459
          |||||||||  ||||||| ||||| || || ||||||||||||||||||||||| || |
Db    301 CAGGATTTTACCGGAAGACCAAACTGGTTGGTTTTCAAGACATGGAGTGTGTGCCCTGCG 360

Qy    460 gagaccctcctcctccttacgaaccgcactgtgcc 494
          ||||||| |||||||| |||||||| |||||| ||
Db    361 GAGACCCACCTCCTCCCTACGAACCACACTGTACC 395


RESULT   3
AL036000
LOCUS       AL036000      282 bp    mRNA            EST       29-FEB-2000
DEFINITION  DKFZp564K1022_r1 564 (synonym: hfbr2) Homo sapiens cDNA clone
            DKFZp564K1022 5', mRNA sequence.
ACCESSION   AL036000
VERSION     AL036000.1  GI:5405629
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 282)
  AUTHORS   Wambutt,R., Heubner,D., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Wambutt, et al.)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Wambutt R
            MIPS
            Am Klopferspitz 18a D-82152 Martinsried, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
            consortium of the German Genome Project.
            s1 sequence also available.
            This clone (DKFZp564K1022) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .282
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="DKFZp564K1022"
                     /clone_lib="564 (synonym: hfbr2)"
                     /tissue_type="brain"
                     /dev_stage="fetal"
                     /lab_host="Xl-2blue"
                     /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"
BASE COUNT       57 a     85 c     75 g     63 t      2 others
ORIGIN


  Query Match             18.4%;  Score 274.8;  DB 28;  Length 282;
  Best Local Similarity   98.6%;  Pred. No. 9.8e-52;
  Matches  276;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy    409 ataggaagacgaaacttgtcggctttcaagacatggagtgtgtgccttgtggagaccctc 468
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3 ATAGGAAGACGAAACTTGTCGGCTTTCAAGACATGGAGTGTGTGCCTTGTGGAGACCCTC  62

Qy    469 ctcctccttacgaaccgcactgtgccagcaaggtcaacctcgtgaagatcgcgtccacgg 528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     63 CTCCTCCTTACGAACCGCACTGTGCCAGCAAGGTCAACCTCGTGAAGATCGCGTCCACGG 122

Qy    529 cctccagcccacgggacacggcgctggctgccgttatctgcagcgctctggccaccgtcc 588
          |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db    123 CCTCCAGCCCACGGGACACGGCGCTGGCTGCCGTTATCTGCANCGCTCTGGCCACCGTCC 182

Qy    589 tgctggccctgctcatcctctgtgtcatctattgtaagagacagtttatggagaagaaac 648
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    183 TGCTGGCCCTGCTCATCCTCTGTGTCATCTATTGTAAGAGACAGTTTATGGAGAAGAAAC 242

Qy    649 ccagctggtctctgcggtcacaggacattcagtacaacgg 688
          |||||||||||||||||| || |||||||||||| ||||
Db    243 CCAGCTGGTCTCTGCGGTCGCANGACATTCAGTACTACGG 282


RESULT   4
BE757704
LOCUS       BE757704      534 bp    mRNA            EST       15-SEP-2000
DEFINITION  212225 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   BE757704
VERSION     BE757704.1  GI:10171696
KEYWORDS    EST.
SOURCE      cow.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 534)
  AUTHORS   Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
            Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
            ,W.W. and Keele,J.W.
  TITLE     Design and use of four pooled tissue normalized cDNA libraries for
            EST discovery in cattle
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 65  row: C  column: 2
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .534
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /clone_lib="MARC 2BOV"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                     Library made from pooled tissue from testis, thymus,
                     semitendonosus muscle, longissimus muscle, pancreas,
                     adrenal, and endometrium."
BASE COUNT      122 a    117 c    171 g    124 t
ORIGIN


  Query Match             17.7%;  Score 264.8;  DB 135;  Length 534;
  Best Local Similarity   82.9%;  Pred. No. 1.9e-49;
  Matches  315;  Conservative    0;  Mismatches   62;  Indels    3;  Gaps    1;

Qy      7 gtagaactctccaacaataaatacatttgataagaaagatggctttaaaagtgctactag 66
          | ||| |||| |||| | |||||||||| ||||||   ||||||| ||| ||||||||
Db    158 GAAGAGCTCTTCAACCAGAAATACATTTAATAAGAGCAATGGCTTCAAACGTGCTACTCA 217

Qy     67 aacaagagaaaacgtttttcactcttttagtattactaggctatttgtcatgtaaagtga 126
            ||| |||||   | ||||||  || |||| ||||||| || |||| |||||  |||||
Db    218 GGCAACAGAAA---TCTTTCACGGTTGTAGTTTTACTAGCCTGTTTGGCATGTGGAGTGA 274

Qy    127 cttgtgaaacaggagactgtagacagcaagaattcagggatcggtctggaaactgtgttc 186
          |||||||||||||||||| ||||||| |||||||||| | ||| |||| ||||||||
Db    275 TTTGTGAAACAGGAGACTGTGGACAGCAGGAATTCAGGGACCAGTCAGGAAGCTGTGTTC 334
```

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Qy     187 cctgcaaccagtgtgggccaggcatggagttgtctaaggaatgtggcttcggctatgggg 246
           ||||| |||||||||||||||||||||||||| |||||||||||||| ||||| ||||
Db     335 TGTGCAAGCAGTGTGGGCCAGGCATGGAGTTGTCCAAGGAATGTGGCTTTGGCTACGGGG 394

Qy     247 aggatgcacagtgtgtgacgtgccggctgcacaggttcaaggaggactggggcttccaga 306
           |||| || |||||||||| |||||||| |||||||||||||||||||||||||  ||||
Db     395 AGGACGCCCAGTGTGTGAAGTGCCGGCCGCACAGGTTCAAGGAGGACTGGGGCTCTCAGA 454

Qy     307 aatgcaagccctgtctggactgcgcagtggtgaaccgctttcagaaggcaaattgttcag 366
           | |||||||| || |||||||||||  || ||| |||||| |||||||| || || || |
Db     455 AGTGCAAGCCGTGCCTGGACTGCGCCCTGCTGAGCCGCTTCCAGAAGGCCAACTGCTCGG 514

Qy     367 ccaccagtgatgccatctgc 386
           ||||  | || ||| |||||
Db     515 CCACTGGCGACGCCGTCTGC 534


RESULT  5
AA003356
LOCUS       AA003356      401 bp    mRNA            EST       19-JUL-1996
DEFINITION  mg49g01.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA
            clone IMAGE:427152 5', mRNA sequence.
ACCESSION   AA003356
VERSION     AA003356.1  GI:1446796
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 401)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:261704
            Seq primer: ETPrimer
            High quality sequence stop: 345.
FEATURES             Location/Qualifiers
     source          1. .401
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:427152"
                     /clone_lib="Soares mouse embryo NbME13.5 14.5"
                     /sex="unknown"
                     /tissue_type="embryo"
                     /dev_stage="13.5-14.5dpc total fetus"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGGAAATTTTTTTTTTTTTTTTTTTTTT
                     T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
                     14.5dpc embryos [total RNA provided by  Minoru Ko, Wayne
                     State Univ., from 2 ]; double-stranded cDNA was ligated to
                     Eco RI adaptors (Pharmacia), digested with Not I and
                     cloned into the Not I and Eco RI sites of the modified
                     pT7T3 vector. Library went through one round of
                     normalization, and was constructed by Bento Soares and
                     M.Fatima Bonaldo.  "

BASE COUNT       92 a     96 c    128 g     85 t
ORIGIN


  Query Match             14.4%;  Score 215.6;  DB 1;  Length 401;
  Best Local Similarity   77.8%;  Pred. No. 2.2e-38;
  Matches  260;  Conservative    0;  Mismatches   74;  Indels    0;  Gaps    0;

Qy      18 caacaataaatacatttgataagaaagatggctttaaaagtgctactagaacaagagaaa 77
           ||  |||||| || |||| | |||   |||||  | || || ||||    |||   ||
Db      68 CAGGAATAAACACGTTTGGTGAGAGCCATGGCACTCAAGGTCCTACCTCTACACAGGACG 127

Qy      78 acgtttttcactcttttagtattactaggctatttgtcatgtaaagtgacttgtgaaaca 137
             | | ||| ||    |  | || |||  | |  || ||||||||||| ||| |||||
Db     128 GTGCTCTTCGCTGCCATTCTCTTCCTACTCCACCTGGCATGTAAAGTGAGTTGCGAAACC 187

Qy     138 ggagactgtagacagcaagaattcagggatcggtctggaaactgtgttccctgcaaccag 197
           ||||| || || |||||| ||||||| |||||| |||||||||||||| | |||||| |||
Db     188 GGAGATTGCAGGCAGCAGGAATTCAAGGATCGATCTGGAAACTGTGTCCTCTGCAAACAG 247

Qy     198 tgtgggccaggcatggagttgtctaaggaatgtggcttcggctatggggaggatgcacag 257
           || || || |||||||||||||| ||||||||||||||||||||||||||||||||||||
Db     248 TGCGGACCTGGCATGGAGTTGTCCAAGGAATGTGGCTTCGGCTATGGGGAGGATGCACAG 307

Qy     258 tgtgtgacgtgccggctgcacaggttcaaggaggactggggcttccagaaatgcaagccc 317
           |||||| | ||| ||| |||| |||||||||| |||||||| |||||||| || |||||
Db     308 TGTGTGCCCTGCAGGCCGCACCGGTTCAAGGAAGACTGGGGTTTCCAGAAGTGTAAGCCA 367

Qy     318 tgtctggactgcgcagtggtgaaccgctttcaga 351
           |||  |||||| ||  |||||||||||| |||||
Db     368 TGTGCGGACTGTGCGCTGGTGAACCGCTGTCAGA 401


RESULT  6
AW478317
LOCUS       AW478317      369 bp    mRNA            EST       07-JUL-2000
DEFINITION  19558 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   AW478317
VERSION     AW478317.1  GI:7048423
KEYWORDS    EST.
SOURCE      cow.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 369)
  AUTHORS   Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
            Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
            ,W.W. and Keele,J.W.
  TITLE     Design and use of four pooled tissue normalized cDNA libraries for
            EST discovery in cattle
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 10  row: M  column: 8
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .369
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /clone_lib="MARC 2BOV"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
```

```
                     /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                     Library made from pooled tissue from testis, thymus,
                     semitendonosus muscle, longissimus muscle, pancreas,
                     adrenal, and endometrium."
BASE COUNT       60 a    115 c    115 g     79 t
ORIGIN


  Query Match             12.9%;  Score 192.8;  DB 91;  Length 369;
  Best Local Similarity   72.9%;  Pred. No. 2.9e-33;
  Matches  248;  Conservative    0;  Mismatches   92;  Indels    0;  Gaps    0;

Qy    780 gggccggtgcgcttgctcccatccatgtgctgtgaggaggcctgcagccccaacccggcg 839
          ||||| || | | |  |||||||| ||||||||  | ||||||| ||     || ||
Db     26 GGGCCAGTCCACCTTGTCCCATCCCGGTGCTGTGGTGGGGCCTGCGGCATTGGCCGGGAC 85

Qy    840 actcttggttgtggggtgcattctgcagccagtcttcaggcaagaaacgcaggcccagcc 899
          |||| |||||||  || ||| |     |||| |||||||  |||||| |||| |||||
Db     86 ACTCCTGGTTGTCAGGGGCACTGCAAGGCCACACTTCAGGACAGAAACACAGGTCCAGCG 145

Qy    900 ggggagatggtgccgacttttcttcggatccctcacgcagtccatctgtggcgagttttca 959
          ||||||  | | || |||||||| || |||||  |   |||| ||||||||||||| |||
Db    146 GGGGAGGCGATTCCCACTTTCTTTGGGTCCCTGTCAAGGTCCCTCTGTGGCGAGTTCTCA 205

Qy    960 gatgcctggcctctgatgcagaatcccatgggtggtgacaacatctctttttgtgactct 1019
          || ||||||||||||||||||||||   |||||||| |  |||| |  || |||||
Db    206 GACGCCTGGCCTCTGATGCAGAATCCCGGTGGTGGTGACGATGTCTCCTCCTGCGACTCC 265

Qy   1020 tatcctgaactcactggagaagacattcattctctcaatccagaacttgaaagctcaacg 1079
          |  ||||| ||| |||||||||||  ||| |||||| | |||||      |||||   |
Db    266 TGCCCTGAGCTCCCTGGAGAAGACGCTCACTCTCTCGACCCAGAGAGCACAAGCTTGGCT 325

Qy   1080 tctttggattcaaatagcagtcaagatttggttggtgggg 1119
          ||  |||| ||| | |||||||  | | |||| |||||||
Db    326 TCCCTGGACTCAGACAGCAGTCGGGGTCTGGTCGGTGGGG 365


RESULT   7
AA036247
LOCUS       AA036247      358 bp    mRNA            EST       26-AUG-1996
DEFINITION  mi74a03.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone
            IMAGE:472300 5', mRNA sequence.
ACCESSION   AA036247
VERSION     AA036247.1  GI:1509376
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 358)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:283044
            Seq primer: -28M13 rev2 from Amersham
            High quality sequence stop: 347.
FEATURES             Location/Qualifiers
     source          1. .358
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:472300"
                     /clone_lib="Soares mouse p3NMF19.5"
                     /dev_stage="19.5 dpc total fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo. RNA was kindly provided by
                     Dr. Minoru Ko (Wayne State University)."
BASE COUNT       81 a     98 c    110 g     69 t
ORIGIN


  Query Match             12.5%;  Score 186.6;  DB 1;  Length 358;
  Best Local Similarity   77.9%;  Pred. No. 7.2e-32;
  Matches  225;  Conservative    0;  Mismatches   64;  Indels    0;  Gaps    0;

Qy     22 aataaatacatttgataagaaagatggctttaaaagtgctactagaacaagagaaaacgt 81
          |||||| || |||| | |||   |||||  | || || ||||    |||   ||    |
Db     69 AATAAACACGTTTGGTGAGAGCCATGGCACTCAAGGTCCTACCTCTACACAGGACGGTGC 128

Qy     82 ttttcactcttttagtattactaggctatttgtcatgtaaagtgacttgtgaaacaggag 141
          | ||| ||     |  | || |||  | |  || ||||||||||| ||| ||||| ||||
Db    129 TCTTCGCTGCCATTCTCTTCCTACTCCACCTGGCATGTAAAGTGAGTTGCGAAACCGGAG 188

Qy    142 actgtagacagcaagaattcagggatcggtctggaaactgtgttccctgcaaccagtgtg 201
          | || || ||||| ||||||| |||||| |||||||||||||| | |||||| ||||| |
Db    189 ATTGCAGGCAGCAGGAATTCAAGGATCGATCTGGAAACTGTGTCCTCTGCAAACAGTGCG 248

Qy    202 ggccaggcatggagttgtctaaggaatgtggcttcggctatggggaggatgcacagtgtg 261
          | || |||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    249 GACCTGGCATGGAGTTGTCCAAGGAATGTGGCTTCGGCTATGGGGAGGATGCACAGTGTG 308

Qy    262 tgacgtgccggctgcacaggttcaaggaggactggggcttccagaaatg 310
          || | ||| ||| |||| |||||||||| |||||||| |||||||| ||
Db    309 TGCCCTGCAGGCCGCACCGGTTCAAGGAAGACTGGGGTTTCCAGAAGTG 357


RESULT   8
BB542020
LOCUS       BB542020      258 bp    mRNA            EST       31-JUL-2000
DEFINITION  BB542020 RIKEN full-length enriched, 0 day neonate eyeball Mus
            musculus cDNA clone E130118G08 3', mRNA sequence.
ACCESSION   BB542020
VERSION     BB542020.1  GI:9613243
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 258)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
            ,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
            Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
            Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
            Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.
            , Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.
            , Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata
            ,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.
            , Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya
            ,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.
            , Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino
            ,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshihide Hayashizaki
            Genome Exploration Research Group, Life Science Tsukuba Center,
```

Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
Email: genome-res@rtc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

```
FEATURES             Location/Qualifiers
     source          1. .258
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="E130118G08"
                     /clone_lib="RIKEN full-length enriched, 0 day neonate
                     eyeball"
                     /tissue_type="eyeball"
                     /dev_stage="0 day neonate"
                     /lab_host="DH10B"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. Second strand cDNA was prepared with the
                     primer adapter of sequence [5'
                     GAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA
                     was cleaved with BamHI and XhoI. Vector: a modified
                     pBluescript KS(+) after bulk excision from Lambda FLC I."
BASE COUNT       55 a     77 c     66 g     60 t
ORIGIN
```

```
  Query Match             10.5%;  Score 157.6;  DB 133;  Length 258;
  Best Local Similarity   80.7%;  Pred. No. 2.3e-25;
  Matches  184;  Conservative    0;  Mismatches   44;  Indels    0;  Gaps    0;

Qy    265 cgtgccggctgcacaggttcaaggaggactggggcttccagaaatgcaagccctgtctgg 324
          | ||| | |  ||| ||||| | || |||||||  |||||||| || ||||| |||  ||
Db      1 CCTGCAGCCCCCACCGGTTCTAAGAAGACTGGGCTTTCCAGAAGTGTAAGCCATGTGCGG 60

Qy    325 actgcgcagtggtgaaccgctttcagaaggcaaattgttcagccaccagtgatgccatct 384
          |||  ||  ||||||||||||||||| | | || || |||  ||||| ||||||  | |
Db     61 ACTTTGCGCTGGTGAACCGCTTTCAGAGGCCCAACTGCTCACACACCACTGATGCTTTTT 120

Qy    385 gcggggactgcttgccaggattttataggaagacgaaacttgtcggctttcaagacatgg 444
          |||||||||||  ||||||||||||  |||||||  |||||  || ||  ||||||||||||
Db    121 GCGGGGACTGCCTGCCAGGATTTTACCGGAAGACCAAACTGGTTGGTTTTCAAGACATGG 180

Qy    445 agtgtgtgccttgtggagaccctcctcctcctcttacgaaccgcactgtg 492
          |||||||  ||  ||||||||  ||||||||  ||||||||  |||||||
Db    181 AGTGTGTCCCCTGCGGAGACCCACCTCCTCCCTACGAACCACACTGTG 228
```

```
RESULT   9
AQ563354
LOCUS       AQ563354      643 bp    DNA             GSS       29-MAY-1999
DEFINITION  HS_5335_B2_B03_T7A RPCI-11 Human Male BAC Library Homo sapiens
            genomic clone Plate=911 Col=6 Row=D, DNA sequence.
ACCESSION   AQ563354
VERSION     AQ563354.1  GI:4922825
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 643)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
            or from Resear h Genetics (info@resgen.com). BAC end Web Server:
            http://www.htsc.washington.edu
            Plate: 911  row: D  column: 6
            Seq primer: T7
            Class: BAC ends
            High quality sequence stop: 643.
FEATURES             Location/Qualifiers
     source          1. .643
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="Plate=911 Col=6 Row=D"
                     /clone_lib="RPCI-11 Human Male BAC Library"
                     /sex="male"
                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                     Male blood DNA was isolated from one randomly chosen donor
                     and partially digested with a combination of EcoRI and
                     EcoRI Methylase. Size selected DNA was cloned into the
                     pBACe3.6 vector at EcoRI sites"
BASE COUNT      151 a    154 c    158 g    167 t     13 others
ORIGIN
```

```
  Query Match             10.4%;  Score 155;  DB 159;  Length 643;
  Best Local Similarity   85.9%;  Pred. No. 1e-24;
  Matches  170;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy    489 tgtgccagcaaggtcaacctcgtgaagatcgcgtccacggcctccagcccacgggacacg 548
          ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db    315 TGTGCCAGCAAGGTCAACCTCGTGAAGATCGCGTNCACGGCCTCCAGCCCACGGGACACG 374

Qy    549 gcgctggctgccgttatctgcagcgctctggccaccgtcctgctggccctgctcatcctc 608
          ||||||     | ||||||||||||||||||||||||||||||||||||||||||||||
Db    375 GCGCTGTGCTGCCGTATCTGCAGCGCTCTGGCCACCGTCCTGCTGGCCCTGCTCATCCTC 434

Qy    609 tgtgtcatctattgtaagagacagtttatggagaagaaacccagctggtctctgcggtca 668
          |||||||||||||||||||||||| ||||||||||||||||||||        |  |
Db    435 TGTGTCATCTATTGTAAGAGACAGTNTATGGAGAAGAAACCCAGCTGTAAGTGTTGAGCT 494

Qy    669 caggacattcagtacaac 686
          ||  ||||    ||  ||
Db    495 CATTACATNTCTTATCAC 512
```

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RESULT 10
AQ544065
LOCUS       AQ544065      646 bp    DNA             GSS       19-MAY-1999
DEFINITION  RPCI-11-315F10.TV RPCI-11 Homo sapiens genomic clone RPCI-11-315F10
            , DNA sequence.
ACCESSION   AQ544065
VERSION     AQ544065.1  GI:4869459
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 646)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
            ,J.C.
  TITLE     Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Other_GSSs: RPCI-11-315F10.TJ
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
            Research Genet cs (info@resgen.com). BAC end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .646
                     /organism="Homo sapiens"
                     /db_xref="GDB:7620705"
                     /db_xref="taxon:9606"
                     /clone="RPCI-11-315F10"
                     /clone_lib="RPCI-11"
                     /sex="Male"
                     /cell_type="Lymphocytes"
                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                     RPCI11 Human Male BAC Library"
BASE COUNT      175 a    135 c    145 g    191 t
ORIGIN


  Query Match             8.4%;  Score 125.8;  DB 159;  Length 646;
  Best Local Similarity   94.9%;  Pred. No. 3.7e-18;
  Matches  130;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy    655 ggtctctgcggtcacaggacattcagtacaacggctctgagctgtcgtgtcttgacagac 714
          ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db    263 GGTCTCTGCGGTCACAGGACATTCAGTACAACGGCTCTGAGCTGTCGTGTTTTGACAGAC 322

Qy    715 ctcagctccacgaatatgcccacagagcctgctgccagtgccgccgtgactcagtgcaga 774
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    323 CTCAGCTCCACGAATATGCCCACAGAGCCTGCTGCCAGTGCCGCCGTGACTCAGTGCAGA 382

Qy    775 cctgcgggccggtgcgc 791
          |||||||   | |  ||
Db    383 CCTGCGGTAAGTTCAGC 399


RESULT 11
AV111112
LOCUS       AV111112      275 bp    mRNA            EST       29-JUN-1999
DEFINITION  AV111112 Mus musculus C57BL/6J 10-day embryo Mus musculus cDNA
            clone 2600016N17, mRNA sequence.
ACCESSION   AV111112
VERSION     AV111112.1  GI:5265192
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 275)
  AUTHORS   Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
            Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara
            ,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,
            Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C.,
            Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara
            ,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N.,
            Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
            Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Chie Owa
            Genome Science Laboratory
            RIKEN
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: 81-298-36-9145
            Fax: 81-298-36-9098
            Email: genome-res@rtc.riken.go.jp
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length cDNA
            (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
            Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
            Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .275
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="2600016N17"
                     /clone_lib="Mus musculus C57BL/6J 10-day embryo"
                     /sex="mixed"
                     /dev_stage="10-day embryo"
BASE COUNT       77 a     86 c     55 g     57 t
ORIGIN


  Query Match             8.3%;  Score 124.4;  DB 31;  Length 275;
  Best Local Similarity   71.3%;  Pred. No. 7e-18;
  Matches  164;  Conservative    0;  Mismatches   66;  Indels    0;  Gaps    0;

Qy    289 aggactggggcttccagaaatgcaagccctgtctggactgcgcagtggtgaaccgctttc 348
          | ||  | || |||||||| |  ||||| |     ||    ||  ||  ||||| || ||
Db     43 AAGAAAGTGGTTTCCAGAAGTAAAAGCCATTCGCCGAACCTGCCCTGTAGAACCCCTATC 102

Qy    349 agaaggcaaattgttcagccaccagtgatgccatctgcggggactgcttgccaggatttt 408
           || | |  |||| |||  ||||| ||||||  ||||||||||||||| ||||| ||||||
Db    103 TGAGGACCCATTGCTCACACACCACTGATGCACTCTGCGGGGACTGCCTGCCAAGATTTT 162

Qy    409 ataggaagacgaaacttgtcggctttcaagacatggagtgtgtgccttgtggagaccctc 468
          |   |||||| ||||| || || ||||||||||||||||||||||| || |||||||| |
Db    163 ACCAGAAGACCAAACTGGTTGGTTTTCAAGACATGGAGTGTGTGCCCTGCGGAGACCCAC 222

Qy    469 ctcctccttacgaaccgcactgtgccagcaaggtcaacctcgtgaagatc 518
          ||||||| |||||||| ||| |||   |    | |||      | ||| |
Db    223 CTCCTCCCTACGAACCACACAGTGAGTGATGTGCCAAGTGGCAGCAGACC 272


RESULT 12
AA495217
LOCUS       AA495217      404 bp    mRNA            EST       27-JUN-1997
DEFINITION  fa04d10.r1 Zebrafish ICRFzfls Danio rerio cDNA clone 10E17 5', mRNA
            sequence.
ACCESSION   AA495217
VERSION     AA495217.1  GI:2225645
KEYWORDS    EST.
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```
SOURCE      zebrafish.
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Rasborinae; Danio.
REFERENCE   1  (bases 1 to 404)
  AUTHORS   Clark,M., Lehrach,H., Appel,B., Eisen,J., Johnson,S., Marra,M.,
            Eddy,S., Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G.,
            Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Martin,J., Moore,B.,
            Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie
            ,T., Waterston,R. and Wilson,R.
  TITLE     WashU Zebrafish EST Project
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Steve Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Steve Johnson lab internal ID - P1_332 NOTE - For this library, the
            CLONE id field represents a position identifier on the original
            cDNA library preparation plate. cDNA Library Preparation: Matthew
            Clark. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by:
            Washington University Genome Sequencing Center Clone distribution:
            Genome Systems, St. Louis, and Max Planck Institut fuer Molekulare
            Genetik, Berlin Tel +49 30 84 13 1235
            Seq primer: T7 ET from Amersham
            High quality sequence stop: 320.
FEATURES             Location/Qualifiers
     source          1. .404
                     /organism="Danio rerio"
                     /db_xref="taxon:7955"
                     /clone="10E17"
                     /clone_lib="Zebrafish ICRFzfls"
                     /sex="mixed"
                     /tissue_type="pooled 26-somite embryos"
                     /lab_host="XL1-blue MRF"
                     /note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; 1st
                     strand cDNA was primed with a Not I - oligo(dT)15 primer
                     [5'pGACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTT3'], on
                     mRNA from pooled 26 somite zebrafish embryos;
                     double-stranded cDNA was ligated to Sal I adaptors (BRL),
                     digested with Not I and cloned into the Not I and Sal I
                     sites of the pSPORT1 vector (BRL). Library was constructed
                     by Matthew Clark (Lehrach lab; ICRF, London and  Max
                     Planck Institut fuer Molekulare Genetik, Berlin) and was
                     not biochemically normalised.  70,000 clones from this
                     library were arrayed on high density filters and
                     subsequently screened by oligonucleotide hybridization
                     fingerprinting to identify unique or minimally redundant
                     clones for more intensive analysis."
BASE COUNT       80 a     98 c    125 g    101 t
ORIGIN
```

```
  Query Match             8.1%;  Score 120.8;  DB 8;  Length 404;
  Best Local Similarity   68.0%;  Pred. No. 4.7e-17;
  Matches  200;  Conservative    0;  Mismatches   87;  Indels    7;  Gaps    2;

Qy    540 cgggacacggcgctggctgccgttatctgcagcgctctggccaccgtcctgctggccctg 599
          || |||| ||| |||||||| || |||||||| |||||||||| ||||| ||||| ||
Db      1 CGAGACATGGCTCTGGCTGCTGTGATCTGCAGTGCTCTGGCCACTGTCCTCCTGGCGCTC 60

Qy    600 ctcatcctctgtgtcatctattgtaagagacagtttatggagaagaaaacccagctggtct 659
          |||||||||||||| ||||| |||||||||||| | ||||||||||||      ||
Db     61 TTCATCCTCTGTGTGATCTACTGTAAGAGACAGCTGCTGGAGAAGAAACC---AGTATCC 117

Qy    660 ctgcggtcacaggacattcagtacaacggctctgagctgtcgtgtcttgacagacctcag 719
          || || | || ||    | || |   ||||| ||| |||| ||| | ||| |      |
Db    118 ATGAGGGCTCATGAGGGCCCGTTCCTGGGCTCGGAGTTGTCTTGTTTGGACCGGAGAGTG 177

Qy    720 ctccacgaatatgcccacagagcctgctgccagtgccgccgtgactcagtgcagacctgc 779
          ||    | |  || ||| ||| ||||||| || |||   | |   ||||  ||||| ||
```

```
Db    178 CT----GGAGTTGTCCAGAGACCCTGCTGTCACTGCACTCATAGATCAGGACAGACGTGT 233

Qy    780 gggccggtgcgcttgctcccatccatgtgctgtgaggaggcctgcagccccaac 833
          ||    || |   || |  | ||  |||| |||||||| | ||| || |  |||
Db    234 GGTGGCGTTCAGCTGGTGTCGTCTGTGTGTTGTGAGGATGTCTGGAGTCAAAAC 287


RESULT  13
AQ514075/c
LOCUS       AQ514075      450 bp    DNA             GSS       05-MAY-1999
DEFINITION  HS_5184_A1_G01_SP6E RPCI-11 Human Male BAC Library Homo sapiens
            genomic clone Plate=760 Col=1 Row=M, DNA sequence.
ACCESSION   AQ514075
VERSION     AQ514075.1  GI:4746366
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 450)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
            or from Resear h Genetics (info@resgen.com). BAC end Web Server:
            http://www.htsc.washington.edu
            Plate: 760  row: M  column: 1
            Seq primer: SP6
            Class: BAC ends
            High quality sequence stop: 450.
FEATURES             Location/Qualifiers
     source          1. .450
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="Plate=760 Col=1 Row=M"
                     /clone_lib="RPCI-11 Human Male BAC Library"
                     /sex="male"
                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                     Male blood DNA was isolated from one randomly chosen donor
                     and partially digested with a combination of EcoRI and
                     EcoRI Methylase. Size selected DNA was cloned into the
                     pBACe3.6 vector at EcoRI sites"
BASE COUNT      156 a     93 c     62 g    137 t      2 others
ORIGIN
```

```
  Query Match             7.6%;  Score 113.8;  DB 158;  Length 450;
  Best Local Similarity   94.4%;  Pred. No. 1.8e-15;
  Matches  118;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy    108 tatttgtcatgtaaagtgacttgtgaaacaggagactgtagacagcaagaattcagggat 167
          |||  |||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db    327 TATCAGTCATGTAAAGTGACTTGTGATACAGGAGACTGTAGACAGCAAGAATTCAGGGAT 268

Qy    168 cggtctggaaactgtgttccctgcaaccagtgtgggccaggcatggagttgtctaaggaa 227
          |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||| |
Db    267 CGGTCTGGAAAATGTGTTCCCTGCAACCAGTGTGGGCCAGGCATGGAGTTGTCTAAGGTA 208

Qy    228 tgtgg 232
```

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          | | |
Db    207 TATTG 203


RESULT 14
CNS05OTC
LOCUS       CNS05OTC     1110 bp    DNA             GSS       26-MAY-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence T3 end of clone
            042M15 of library C from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL347097
VERSION     AL347097.1  GI:8240867
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis.
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;
            Holacanthopterygii; Acanthopterygii; Percomorpha;
            Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Tetraodon.
REFERENCE   1  (bases 1 to 1110)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
            Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
  TITLE     Charaterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1110)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 1110)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .1110
                     /organism="Tetraodon nigroviridis"
                     /db_xref="taxon:99883"
                     /clone="042M15"
                     /clone_lib="C"
                     /note="Genoscope sequence ID : C0BC042AG08T1-end : T3"
BASE COUNT      222 a    293 c    292 g    281 t     22 others
ORIGIN


  Query Match             6.4%;  Score 95;  DB 193;  Length 1110;
  Best Local Similarity   70.6%;  Pred. No. 3.4e-11;
  Matches  139;  Conservative    0;  Mismatches   57;  Indels    1;  Gaps    1;

Qy    223 aggaatgtggcttcggctatggggaggatgcacagtgtgtgacgtgccggctgcacaggt 282
          |||||||||||||| ||||| || |||||||| | ||||||| | || |||     | | |
Db    706 AGGAATGTGGCTTTGGCTACGGAGAGGATGCCCGGTGTGTGCCCTGTCGGAGCGGCCGCT 765

Qy    283 tcaaggaggactggggcttccagaaatgcaagccctgtctggactgcgcagtggtgaacc 342
          |||| |||||  | ||  | ||||| |||||| |||| ||||||||||   |  | ||||
Db    766 TCAAAGAGGAGCGCGGNCTGCAGAAGTGCAAGGCCTGCCTGGACTGCGGGCTCATCAACC 825

Qy    343 gctttcagaaggcaaattgttcagccaccagtgatgccatct-gcggggactgcttgcca 401
          |||| |||||||| || || ||  ||| |||  | ||  | | | || |||||| ||||
Db    826 GCTTCCAGAAGGCCAACTGCTCCACCAGCAGCAACGCAGTNGGTGGAGACTGCCTGCCC 885

Qy    402 ggattttataggaagac 418
          || |     || | | |
Db    886 GGGTCAGTCAGCAGGCC 902
```

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RESULT 15
AW527025/c
LOCUS       AW527025      414 bp    mRNA            EST       06-MAR-2000
DEFINITION  UI-R-BO1-ajg-f-10-0-UI.s1 UI-R-BO1 Rattus norvegicus cDNA clone
            UI-R-BO1-ajg-f-10-0-UI 3', mRNA sequence.
ACCESSION   AW527025
VERSION     AW527025.1  GI:7169439
KEYWORDS    EST.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 414)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: msoares@blue.weeg.uiowa.edu
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. The sequence tag present in the cDNA between the NotI site
            and the oligo-dT track served to identify it as a clone from the
            normalized mid-brain library cDNA Library Preparation: M.B. Soares
            Lab Clone distribution: clones will be available through Research
            Genetics (www.resgen.com)
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .414
                     /organism="Rattus norvegicus"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /clone="UI-R-BO1-ajg-f-10-0-UI"
                     /clone_lib="UI-R-BO1"
                     /dev_stage="adult"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The library
                     (UI-R-BO1) is a subtracted library derived from a mixture
                     of the following tissues: thalamus, cerebellum,
                     hypothalamus, medulla, pons, midbrain, cerebral cortex,
                     corpus striatum and hippocampus. For a detailed
                     description of the library from which this clone was
                     derived, please visit our web site at
                     ratest.eng.uiowa.edu. The subtraction has been previously
                     described in (Bonaldo, Lennon and Soares, Genome Research
                     6:791-806, 1996)
                     TAG_LIB=UI-R-BO1
                     TAG_TISSUE=mid-brain
                     TAG_SEQ=GATGG"
BASE COUNT       91 a    102 c     94 g    127 t
ORIGIN


  Query Match             6.1%;  Score 91.2;  DB 91;  Length 414;
  Best Local Similarity   58.5%;  Pred. No. 2.2e-10;
  Matches  159;  Conservative    0;  Mismatches  113;  Indels    0;  Gaps    0;

Qy   1019 ttatcctgaactcactggagaagacattcattctctcaatccagaacttgaaagctcaac 1078
          |||||||||||||||||||||||| ||  |||| |||||||| |||  ||||||||||||
Db    414 TTATCCTGAACTCACTGGAGAAGATATCAATTCCCTCAATCCCGAAAATGAAAGCTCAAC 355

Qy   1079 gtctttggattcaaatagcagtcaagatttggttggtggggctgttccagtccagtctca 1138
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          ||| ||||||| ||| |  |||| ||| ||| ||| |  |||| |||||     |||
Db    354 ATCTGTGGATTCCAATGGTGGTCAGGATCTGGCTGGGGCAGCTGCTCCAGATTCTTCTGG 295

Qy   1139 ttctgaaaactttacagcagctactgatttatctagatataacaacacactggtagaatc 1198
            |         |   | |   |   |  || | |  |   | | ||  |    ||
Db    294 AGATTTTTCAGAAAATACTGACTCACCTAGATATGGTGACGCCGATACGGTCTGGGAGCA 235

Qy   1199 agcatcaactcaggatgcactaactatgagaagccagctagatcaggagagtggcgctat 1258
          | |   | ||||||||||| | ||  |    ||||      |    |||     | |  |
Db    234 AACCCTAGCTCAGGATGCTCAAAGGACTCCAAGCAGAGAGGGCTGGGAAGCCAGTGAAAA 175

Qy   1259 catccacccagccactcagacgtccctccagg 1290
          | |  | | ||||||    ||  || ||||||
Db    174 CCTGAATCTAGCCACGTCCACAGCCTTCCAGG 143


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Job time: 21827 sec
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